



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant	:	Baker et al.)	Group Art Unit Unknown
)	
Appl. No.	:	10/015,715)	
)	
Filed	:	December 12, 2001)	
)	
For	:	SECRETED AND)	
		TRANSMEMBRANE)	
		POLYPEPTIDES AND NUCLEIC)	
		ACIDS ENCODING THE SAME)	
)	
Examiner	:	Unknown)	

SEQUENCE SUBMISSION STATEMENT

United States Patent and Trademark Office
 PO Box 2327
 Arlington, VA 22202

Dear Sir:

This is in response to the Notice to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures, mailed March 20, 2002. I hereby state that the amendments, made in accordance with 37 C.F.R. § 1.825(a) and included in the Substitute Sequence Listing submitted herewith, are supported in the application, and that the Substitute Sequence Listing does not include new matter.

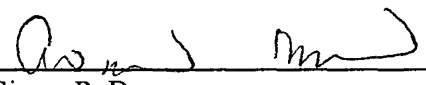
I further state that the information recorded in the currently submitted substitute copy of the computer-readable form of the Sequence Listing is identical to the paper form of the Sequence Listing submitted herewith as required in 37 C.F.R. § 1.825(b).

Please charge any additional fees, including any fees for additional extension of time, or credit overpayment to Deposit Account No. 11-1410.

Respectfully submitted,

KNOBBE, MARTENS, OLSON & BEAR, LLP

Dated: June 20, 2002

By: 
 Ginger R. Dreger
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 620 Newport Center Drive, 16th Floor
 Newport Beach, CA 92660
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#5

Sequence Listing



<110> Baker, Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan l.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
Pan, James
Paoni, Nicholas F.

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tacattttta tcaactggatg tgactcgggc tttggaaact tggcagccag 250
aacttttgat aaaaagggat ttcattgtaat cgctgcctgt ctgactgaat 300
caggatcaac agcttttaag gcagaaacct cagagagact tcgtactgtg 350
cttctggatg tgaccgaccc agagaatgtc aagaggactg cccagtgggt 400
gaagaaccaa gttggggaga aaggctctctg gggctctgat aataatgctg 450
gtgttcccgg cgtgctggct cccactgact ggctgacact agaggactac 500
agagaaccta ttgaagtga cctgtttgga ctcatcagtg tgacactaaa 550
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gtgttggagg tcgccttgca atcgttggag ggggctatac tccatccaaa 650
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gtatttaggc tttgctgct tgggtgtgat taagggaat tgaaagactt 1350
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<210> 10
<211> 319
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-17
<223> Signal Peptide

<220>
<221> misc_feature
<222> 36-47, 108-113, 166-171, 198-203, 207-212
<223> N-myristoylation Sites.

<220>
<221> misc_feature
<222> 39-42
<223> Glycosaminoglycan Attachment Site.

<220>
<221> TRANSMEM
<222> 136-152
<223> Transmembrane Domain

<220>
<221> misc_feature
<222> 161-163, 187-190 and 253-256
<223> N-glycosylation Sites.

<400> 10
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1 5 10 15

Trp Thr Arg Lys Gly Lys Leu Lys Ile Glu Asp Ile Thr Asp Lys
20 25 30

Tyr Ile Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Ala
35 40 45

Ala Arg Thr Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys
50 55 60

Leu Thr Glu Ser Gly Ser Thr Ala Leu Lys Ala Glu Thr Ser Glu
65 70 75

Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu Asn Val
80 85 90

Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys Gly
95 100 105

Leu Trp Gly Leu Ile Asn Asn Ala Gly Val Pro Gly Val Leu Ala
110 115 120

Pro Thr Asp Trp Leu Thr Leu Glu Asp Tyr Arg Glu Pro Ile Glu	125	130	135
Val Asn Leu Phe Gly Leu Ile Ser Val Thr Leu Asn Met Leu Pro	140	145	150
Leu Val Lys Lys Ala Gln Gly Arg Val Ile Asn Val Ser Ser Val	155	160	165
Gly Gly Arg Leu Ala Ile Val Gly Gly Gly Tyr Thr Pro Ser Lys	170	175	180
Tyr Ala Val Glu Gly Phe Asn Asp Ser Leu Arg Arg Asp Met Lys	185	190	195
Ala Phe Gly Val His Val Ser Cys Ile Glu Pro Gly Leu Phe Lys	200	205	210
Thr Asn Leu Ala Asp Pro Val Lys Val Ile Glu Lys Lys Leu Ala	215	220	225
Ile Trp Glu Gln Leu Ser Pro Asp Ile Lys Gln Gln Tyr Gly Glu	230	235	240
Gly Tyr Ile Glu Lys Ser Leu Asp Lys Leu Lys Gly Asn Lys Ser	245	250	255
Tyr Val Asn Met Asp Leu Ser Pro Val Val Glu Cys Met Asp His	260	265	270
Ala Leu Thr Ser Leu Phe Pro Lys Thr His Tyr Ala Ala Gly Lys	275	280	285
Asp Ala Lys Ile Phe Trp Ile Pro Leu Ser His Met Pro Ala Ala	290	295	300
Leu Gln Asp Phe Leu Leu Leu Lys Gln Lys Ala Glu Leu Ala Asn	305	310	315
Pro Lys Ala Val			

<210> 11
 <211> 2720
 <212> DNA
 <213> Homo sapiens

<400> 11
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 gccccttggg ccgtcgccac cactgtagtc atgtaccac cgccgccgcc 150
 gccgcctcat cgggacttca tctcggtgac gctgagcttt ggcgagagct 200

atgacaacag caagagttgg cggcggcgct cgtgctggag gaaatggaag 250
caactgtoga gattgcagcg gaatatgatt ctcttctctc ttgcctttct 300
gcttttctgt ggactcctct tctacatcaa cttggctgac cattggaaag 350
ctctggcttt caggctagag gaagagcaga agatgaggcc agaaattgct 400
gggttaaaac cagcaaattc acccgtctta ccagctctc agaaggcgga 450
caccgaccct gagaacttac ctgagatttc gtcacagaag acacaaagac 500
acatccagcg gggaccacct cacctgcaga ttagaccccc aagccaagac 550
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ggatccccgc ccggaaggag atccgcagag gacagtcctc agctggaggg 650
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gaagtgccca ccaagcctcc cctgccaccg gccaggacac agggcacacc 750
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gtgtccaggt ccttcagtga gtggtttggc ctcggtctca cactgatcga 900
cgcgctggac accatgtgga tcttgggtct gaggaagaa tttgaggaag 950
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gtctcacagg ggataagaag tttcaggagg cagtggagaa ggtgacacag 1300
cacatccacg gcctgtctgg gaagaaggat gggctggtgc ccatgttcat 1350
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ccagggccga cagctactat gactacctgc tgaagcagtg gatccagggc 1450
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cagccacatg gagctggccc aggagctcat ggagacttgt taccagatga 1700
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 tcacagggga cgcgaaatac caggactggg gctgggagat tctgcagagc 1900
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 ttgatttgct ctaaccgcaa 2720

<210> 12

<211> 699

<212> PRT

<213> Homo sapiens

<220>

<221> TRANSMEM

<222> 21-40 and 84-105

<223> Transmembrane Domain (type II)

<400> 12

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	20	25	30
Val Ala Thr Thr	Val Val Met Tyr Pro	Pro Pro Pro Pro	Pro
	35	40	45
His Arg Asp Phe	Ile Ser Val Thr Leu	Ser Phe Gly Glu Ser	Tyr
	50	55	60
Asp Asn Ser Lys	Ser Trp Arg Arg Arg	Ser Cys Trp Arg Lys	Trp
	65	70	75
Lys Gln Leu Ser	Arg Leu Gln Arg Asn	Met Ile Leu Phe Leu	Leu
	80	85	90
Ala Phe Leu Leu	Phe Cys Gly Leu Leu	Phe Tyr Ile Asn Leu	Ala
	95	100	105
Asp His Trp Lys	Ala Leu Ala Phe Arg	Leu Glu Glu Glu Gln	Lys
	110	115	120
Met Arg Pro Glu	Ile Ala Gly Leu Lys	Pro Ala Asn Pro Pro	Val
	125	130	135
Leu Pro Ala Pro	Gln Lys Ala Asp Thr	Asp Pro Glu Asn Leu	Pro
	140	145	150
Glu Ile Ser Ser	Gln Lys Thr Gln Arg	His Ile Gln Arg Gly	Pro
	155	160	165
Pro His Leu Gln	Ile Arg Pro Pro Ser	Gln Asp Leu Lys Asp	Gly
	170	175	180
Thr Gln Glu Glu	Ala Thr Lys Arg Gln	Glu Ala Pro Val Asp	Pro
	185	190	195
Arg Pro Glu Gly	Asp Pro Gln Arg Thr	Val Ile Ser Trp Arg	Gly
	200	205	210
Ala Val Ile Glu	Pro Glu Gln Gly Thr	Glu Leu Pro Ser Arg	Arg
	215	220	225
Ala Glu Val Pro	Thr Lys Pro Pro Leu	Pro Pro Ala Arg Thr	Gln
	230	235	240
Gly Thr Pro Val	His Leu Asn Tyr Arg	Gln Lys Gly Val Ile	Asp
	245	250	255
Val Phe Leu His	Ala Trp Lys Gly Tyr	Arg Lys Phe Ala Trp	Gly
	260	265	270
His Asp Glu Leu	Lys Pro Val Ser Arg	Ser Phe Ser Glu Trp	Phe
	275	280	285
Gly Leu Gly Leu	Thr Leu Ile Asp Ala	Leu Asp Thr Met Trp	Ile

290										295					300				
Leu	Gly	Leu	Arg	Lys	Glu	Phe	Glu	Glu	Ala	Arg	Lys	Trp	Val	Ser					
				305					310					315					
Lys	Lys	Leu	His	Phe	Glu	Lys	Asp	Val	Asp	Val	Asn	Leu	Phe	Glu					
				320					325					330					
Ser	Thr	Ile	Arg	Ile	Leu	Gly	Gly	Leu	Leu	Ser	Ala	Tyr	His	Leu					
				335					340					345					
Ser	Gly	Asp	Ser	Leu	Phe	Leu	Arg	Lys	Ala	Glu	Asp	Phe	Gly	Asn					
				350					355					360					
Arg	Leu	Met	Pro	Ala	Phe	Arg	Thr	Pro	Ser	Lys	Ile	Pro	Tyr	Ser					
				365					370					375					
Asp	Val	Asn	Ile	Gly	Thr	Gly	Val	Ala	His	Pro	Pro	Arg	Trp	Thr					
				380					385					390					
Ser	Asp	Ser	Thr	Val	Ala	Glu	Val	Thr	Ser	Ile	Gln	Leu	Glu	Phe					
				395					400					405					
Arg	Glu	Leu	Ser	Arg	Leu	Thr	Gly	Asp	Lys	Lys	Phe	Gln	Glu	Ala					
				410					415					420					
Val	Glu	Lys	Val	Thr	Gln	His	Ile	His	Gly	Leu	Ser	Gly	Lys	Lys					
				425					430					435					
Asp	Gly	Leu	Val	Pro	Met	Phe	Ile	Asn	Thr	His	Ser	Gly	Leu	Phe					
				440					445					450					
Thr	His	Leu	Gly	Val	Phe	Thr	Leu	Gly	Ala	Arg	Ala	Asp	Ser	Tyr					
				455					460					465					
Tyr	Glu	Tyr	Leu	Leu	Lys	Gln	Trp	Ile	Gln	Gly	Gly	Lys	Gln	Glu					
				470					475					480					
Thr	Gln	Leu	Leu	Glu	Asp	Tyr	Val	Glu	Ala	Ile	Glu	Gly	Val	Arg					
				485					490					495					
Thr	His	Leu	Leu	Arg	His	Ser	Glu	Pro	Ser	Lys	Leu	Thr	Phe	Val					
				500					505					510					
Gly	Glu	Leu	Ala	His	Gly	Arg	Phe	Ser	Ala	Lys	Met	Asp	His	Leu					
				515					520					525					
Val	Cys	Phe	Leu	Pro	Gly	Thr	Leu	Ala	Leu	Gly	Val	Tyr	His	Gly					
				530					535					540					
Leu	Pro	Ala	Ser	His	Met	Glu	Leu	Ala	Gln	Glu	Leu	Met	Glu	Thr					
				545					550					555					
Cys	Tyr	Gln	Met	Asn	Arg	Gln	Met	Glu	Thr	Gly	Leu	Ser	Pro	Glu					
				560					565					570					
Ile	Val	His	Phe	Asn	Leu	Tyr	Pro	Gln	Pro	Gly	Arg	Arg	Asp	Val					

575										580					585				
Glu	Val	Lys	Pro	Ala	Asp	Arg	His	Asn	Leu	Leu	Arg	Pro	Glu	Thr					
				590					595					600					
Val	Glu	Ser	Leu	Phe	Tyr	Leu	Tyr	Arg	Val	Thr	Gly	Asp	Arg	Lys					
				605					610					615					
Tyr	Gln	Asp	Trp	Gly	Trp	Glu	Ile	Leu	Gln	Ser	Phe	Ser	Arg	Phe					
				620					625					630					
Thr	Arg	Val	Pro	Ser	Gly	Gly	Tyr	Ser	Ser	Ile	Asn	Asn	Val	Gln					
				635					640					645					
Asp	Pro	Gln	Lys	Pro	Glu	Pro	Arg	Asp	Lys	Met	Glu	Ser	Phe	Phe					
				650					655					660					
Leu	Gly	Glu	Thr	Leu	Lys	Tyr	Leu	Phe	Leu	Leu	Phe	Ser	Asp	Asp					
				665					670					675					
Pro	Asn	Leu	Leu	Ser	Leu	Asp	Ala	Tyr	Val	Phe	Asn	Thr	Glu	Ala					
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His	Pro	Leu	Pro	Ile	Trp	Thr	Pro	Ala											
				695															

<210> 13

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 13

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<210> 14

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 14

ccatccttct tcccagacag gccg 24

<210> 15

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 15

gaagcctgtg tccaggtcct tcagtgagtg gtttggcctc ggtc 44

<210> 16

<211> 1524

<212> DNA

<213> Homo sapiens

<400> 16

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ccctcggaag tgttccgtct tccacctgtt cgtggcctgc ctctcgctgg 200
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 cctactctga cctccttcac gtgcccaggc ctgtgggtag tggggagggc 1450
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<210> 17
 <211> 327
 <212> PRT
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 1-42
 <223> Signal peptide.

<220>
 <221> misc_feature
 <222> 19-25,65-71,247-253,285-291,303-310
 <223> N-myristoylation site.

<220>
 <221> misc_feature
 <222> 27-31
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>
 <221> TRANSMEM
 <222> 29-49
 <223> Transmembrane domain (type II).

<220>
 <221> misc_feature
 <222> 154-158
 <223> N-glycosylation site.

<220>
 <221> misc_feature
 <222> 226-233
 <223> Tyrosine kinase phosphorylation site.

<400> 17
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 Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser
 20 25 30
 Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser
 35 40 45

Leu	Leu	Trp	Leu	Gln	Leu	Ser	Cys	Ser	Gly	Asp	Val	Ala	Arg	Ala				50	55	60
Val	Arg	Gly	Gln	Gly	Gln	Glu	Thr	Ser	Gly	Pro	Pro	Arg	Ala	Cys				65	70	75
Pro	Pro	Glu	Pro	Pro	Pro	Glu	His	Trp	Glu	Glu	Asp	Ala	Ser	Trp				80	85	90
Gly	Pro	His	Arg	Leu	Ala	Val	Leu	Val	Pro	Phe	Arg	Glu	Arg	Phe				95	100	105
Glu	Glu	Leu	Leu	Val	Phe	Val	Pro	His	Met	Arg	Arg	Phe	Leu	Ser				110	115	120
Arg	Lys	Lys	Ile	Arg	His	His	Ile	Tyr	Val	Leu	Asn	Gln	Val	Asp				125	130	135
His	Phe	Arg	Phe	Asn	Arg	Ala	Ala	Leu	Ile	Asn	Val	Gly	Phe	Leu				140	145	150
Glu	Ser	Ser	Asn	Ser	Thr	Asp	Tyr	Ile	Ala	Met	His	Asp	Val	Asp				155	160	165
Leu	Leu	Pro	Leu	Asn	Glu	Glu	Leu	Asp	Tyr	Gly	Phe	Pro	Glu	Ala				170	175	180
Gly	Pro	Phe	His	Val	Ala	Ser	Pro	Glu	Leu	His	Pro	Leu	Tyr	His				185	190	195
Tyr	Lys	Thr	Tyr	Val	Gly	Gly	Ile	Leu	Leu	Leu	Ser	Lys	Gln	His				200	205	210
Tyr	Arg	Leu	Cys	Asn	Gly	Met	Ser	Asn	Arg	Phe	Trp	Gly	Trp	Gly				215	220	225
Arg	Glu	Asp	Asp	Glu	Phe	Tyr	Arg	Arg	Ile	Lys	Gly	Ala	Gly	Leu				230	235	240
Gln	Leu	Phe	Arg	Pro	Ser	Gly	Ile	Thr	Thr	Gly	Tyr	Lys	Thr	Phe				245	250	255
Arg	His	Leu	His	Asp	Pro	Ala	Trp	Arg	Lys	Arg	Asp	Gln	Lys	Arg				260	265	270
Ile	Ala	Ala	Gln	Lys	Gln	Glu	Gln	Phe	Lys	Val	Asp	Arg	Glu	Gly				275	280	285
Gly	Leu	Asn	Thr	Val	Lys	Tyr	His	Val	Ala	Ser	Arg	Thr	Ala	Leu				290	295	300
Ser	Val	Gly	Gly	Ala	Pro	Cys	Thr	Val	Leu	Asn	Ile	Met	Leu	Asp				305	310	315
Cys	Asp	Lys	Thr	Ala	Thr	Pro	Trp	Cys	Thr	Phe	Ser							320	325	

<210> 18
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 18
gcgaacgctt cgaggagtc tgg 23

<210> 19
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 19
gcagtgcggg aagccacatg gtac 24

<210> 20
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 20
cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21
<211> 494
<212> DNA
<213> Homo sapiens

<400> 21
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gactggtcgg tgcccagaaa gtctcttctg ccaactgacgc ccccatcagg 150
gattgggcct tctttccccc ttcttttctg tgtctctctgc ctcatcggcc 200
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<210> 22
<211> 73
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-15
<223> Signal peptide.

<220>
<221> misc_feature
<222> 3-18
<223> Growth factor and cytokines receptors family.

<400> 22
Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Leu Leu Lys Gly
1 5 10 15
Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser
20 25 30
Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser
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50 55 60
Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly
65 70

<210> 23
<211> 2883
<212> DNA
<213> Homo sapiens

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ccataaggct cgggtcgccg ctggggccgc gccgcgctcc tgcccgcccg 150
ggctccgggg cggcccgcta ggccagtgcg ccgcgcgctc cccgcagggc 200
cccggcccg cagcatggagc caccgggacg ccggcggggc cgcgcgcagc 250
cgccgctgtt gctgccgctc tcgctgttag cgctgctcgc gctgctggga 300
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tgggcgggcc cgaggggctg gcagggcggc gggcgccgcc gagggcaagg 400
tggtgtgcag cagcctggaa ctgcgcgagg tcctgcccc agataactctg 450

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gaagaatggc tcattttctg ggttaagtct ccttgaaaga ttggacctcc 550
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<210> 24
<211> 616
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-33
<223> Signal peptide.

<220>
<221> TRANSMEM
<222> 13-40
<223> Transmembrane domain (type II).

<400> 24

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			20					25						30	
Gly	Gly	Gly	Gly	Gly	Ala	Ala	Ala	Leu	Pro	Ala	Gly	Cys	Lys	His	
			35					40						45	
Asp	Gly	Arg	Pro	Arg	Gly	Ala	Gly	Arg	Ala	Ala	Gly	Ala	Ala	Glu	
			50					55						60	
Gly	Lys	Val	Val	Cys	Ser	Ser	Leu	Glu	Leu	Ala	Gln	Val	Leu	Pro	
			65					70						75	
Pro	Asp	Thr	Leu	Pro	Asn	Arg	Thr	Val	Thr	Leu	Ile	Leu	Ser	Asn	
			80					85						90	
Asn	Lys	Ile	Ser	Glu	Leu	Lys	Asn	Gly	Ser	Phe	Ser	Gly	Leu	Ser	
			95					100						105	
Leu	Leu	Glu	Arg	Leu	Asp	Leu	Arg	Asn	Asn	Leu	Ile	Ser	Ser	Ile	
			110					115						120	
Asp	Pro	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Ser	Leu	Lys	Arg	Leu	Asp	
			125					130						135	
Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg	
			140					145						150	
Gly	Leu	Thr	Asn	Leu	Val	Arg	Leu	Asn	Leu	Ser	Gly	Asn	Leu	Phe	
			155					160						165	
Ser	Ser	Leu	Ser	Gln	Gly	Thr	Phe	Asp	Tyr	Leu	Ala	Ser	Leu	Arg	
			170					175						180	
Ser	Leu	Glu	Phe	Gln	Thr	Glu	Tyr	Leu	Leu	Cys	Asp	Cys	Asn	Ile	
			185					190						195	
Leu	Trp	Met	His	Arg	Trp	Val	Lys	Glu	Lys	Asn	Ile	Thr	Val	Arg	
			200					205						210	
Asp	Thr	Arg	Cys	Val	Tyr	Pro	Lys	Ser	Leu	Gln	Ala	Gln	Pro	Val	
			215					220						225	
Thr	Gly	Val	Lys	Gln	Glu	Leu	Leu	Thr	Cys	Asp	Pro	Pro	Leu	Glu	
			230					235						240	
Leu	Pro	Ser	Phe	Tyr	Met	Thr	Pro	Ser	His	Arg	Gln	Val	Val	Phe	
			245					250						255	
Glu	Gly	Asp	Ser	Leu	Pro	Phe	Gln	Cys	Met	Ala	Ser	Tyr	Ile	Asp	
			260					265						270	
Gln	Asp	Met	Gln	Val	Leu	Trp	Tyr	Gln	Asp	Gly	Arg	Ile	Val	Glu	
			275					280						285	

Thr Asp Glu Ser	Gln Gly Ile Phe Val	Glu Lys Asn Met Ile His
290	295	300
Asn Cys Ser Leu	Ile Ala Ser Ala Leu Thr	Ile Ser Asn Ile Gln
305	310	315
Ala Gly Ser Thr	Gly Asn Trp Gly Cys His	Val Gln Thr Lys Arg
320	325	330
Gly Asn Asn Thr	Arg Thr Val Asp Ile	Val Val Leu Glu Ser Ser
335	340	345
Ala Gln Tyr Cys	Pro Pro Glu Arg Val	Val Asn Asn Lys Gly Asp
350	355	360
Phe Arg Trp Pro	Arg Thr Leu Ala Gly	Ile Thr Ala Tyr Leu Gln
365	370	375
Cys Thr Arg Asn	Thr His Gly Ser Gly	Ile Tyr Pro Gly Asn Pro
380	385	390
Gln Asp Glu Arg	Lys Ala Trp Arg Arg	Cys Asp Arg Gly Gly Phe
395	400	405
Trp Ala Asp Asp	Asp Tyr Ser Arg Cys	Gln Tyr Ala Asn Asp Val
410	415	420
Thr Arg Val Leu	Tyr Met Phe Asn Gln	Met Pro Leu Asn Leu Thr
425	430	435
Asn Ala Val Ala	Thr Ala Arg Gln Leu	Leu Ala Tyr Thr Val Glu
440	445	450
Ala Ala Asn Phe	Ser Asp Lys Met Asp	Val Ile Phe Val Ala Glu
455	460	465
Met Ile Glu Lys	Phe Gly Arg Phe Thr	Lys Glu Glu Lys Ser Lys
470	475	480
Glu Leu Gly Asp	Val Met Val Asp Ile	Ala Ser Asn Ile Met Leu
485	490	495
Ala Asp Glu Arg	Val Leu Trp Leu Ala	Gln Arg Glu Ala Lys Ala
500	505	510
Cys Ser Arg Ile	Val Gln Cys Leu Gln	Arg Ile Ala Thr Tyr Arg
515	520	525
Leu Ala Gly Gly	Ala His Val Tyr Ser	Thr Tyr Ser Pro Asn Ile
530	535	540
Ala Leu Glu Ala	Tyr Val Ile Lys Ser	Thr Gly Phe Thr Gly Met
545	550	555
Thr Cys Thr Val	Phe Gln Lys Val Ala	Ala Ser Asp Arg Thr Gly
560	565	570

Leu Ser Asp Tyr Gly Arg Arg Asp Pro Glu Gly Asn Leu Asp Lys
575 580 585

Gln Leu Ser Phe Lys Cys Asn Val Ser Asn Thr Phe Ser Ser Leu
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Ala Leu Lys Val Cys Tyr Ile Leu Gln Ser Phe Lys Thr Ile Tyr
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Ser

<210> 25

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 25

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<210> 26

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 26

aactggaaag gaaggctgtc tccc 24

<210> 27

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 27

gtaaaggaga agaacatcac ggtacgggat accaggtgtg tttatcctaa 50

<210> 28

<211> 683

<212> DNA

<213> Homo sapiens

<400> 28

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gcagaggctt cgtgaaggag ttatcagaga cattgagagg caaatcggga 150

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<210> 29
 <211> 81
 <212> PRT
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 1-21
 <223> Signal peptide.

<400> 29
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 Thr Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp
 20 25 30
 Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln
 35 40 45
 Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile
 50 55 60
 Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala
 65 70 75
 Lys Gly Ser Gln Lys Ser
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<210> 30
 <211> 2128
 <212> DNA
 <213> Homo sapiens

<400> 30

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<210> 31

<211> 322

<212> PRT

<213> Homo sapiens

<400> 31

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				20					25					30
Ala	Leu	Thr	Gln	Pro	Leu	Gly	Leu	Leu	Arg	Leu	Leu	Gln	Leu	Val
				35					40					45
Ser	Thr	Cys	Val	Ala	Phe	Ser	Leu	Val	Ala	Ser	Val	Gly	Ala	Trp
				50					55					60
Thr	Gly	Ser	Met	Gly	Asn	Trp	Ser	Met	Phe	Thr	Trp	Cys	Phe	Cys
				65					70					75
Phe	Ser	Val	Thr	Leu	Ile	Ile	Leu	Ile	Val	Glu	Leu	Cys	Gly	Leu
				80					85					90
Gln	Ala	Arg	Phe	Pro	Leu	Ser	Trp	Arg	Asn	Phe	Pro	Ile	Thr	Phe
				95					100					105

Ala Cys Tyr Ala	Ala Leu Phe Cys Leu	Ser Ala Ser Ile Ile Tyr	
	110	115	120
Pro Thr Thr Tyr	Val Gln Phe Leu Ser	His Gly Arg Ser Arg Asp	
	125	130	135
His Ala Ile Ala	Ala Thr Phe Phe Ser	Cys Ile Ala Cys Val Ala	
	140	145	150
Tyr Ala Thr Glu	Val Ala Trp Thr Arg	Ala Arg Pro Gly Glu Ile	
	155	160	165
Thr Gly Tyr Met	Ala Thr Val Pro Gly	Leu Leu Lys Val Leu Glu	
	170	175	180
Thr Phe Val Ala	Cys Ile Ile Phe Ala	Phe Ile Ser Asp Pro Asn	
	185	190	195
Leu Tyr Gln His	Gln Pro Ala Leu Glu	Trp Cys Val Ala Val Tyr	
	200	205	210
Ala Ile Cys Phe	Ile Leu Ala Ala Ile	Ala Ile Leu Leu Asn Leu	
	215	220	225
Gly Glu Cys Thr	Asn Val Leu Pro Ile	Pro Phe Pro Ser Phe Leu	
	230	235	240
Ser Gly Leu Ala	Leu Leu Ser Val Leu	Leu Tyr Ala Thr Ala Leu	
	245	250	255
Val Leu Trp Pro	Leu Tyr Gln Phe Asp	Glu Lys Tyr Gly Gly Gln	
	260	265	270
Pro Arg Arg Ser	Arg Asp Val Ser Cys	Ser Arg Ser His Ala Tyr	
	275	280	285
Tyr Val Cys Ala	Trp Asp Arg Arg Leu	Ala Val Ala Ile Leu Thr	
	290	295	300
Ala Ile Asn Leu	Leu Ala Tyr Val Ala	Asp Leu Val His Ser Ala	
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His Leu Val Phe	Val Lys Val		
	320		

<210> 32

<211> 3680

<212> DNA

<213> Homo sapiens

<400> 32

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<210> 33

<211> 335

<212> PRT

<213> Homo sapiens

<400> 33

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Phe	Gly	Thr	Val	Ser	Cys	Glu	Tyr	Met	Leu	Gly	Ser	Pro	Leu	Ser
				20					25					30
Ser	Leu	Ala	Gln	Val	Asn	Leu	Ser	Pro	Phe	Ser	His	Pro	Lys	Val
				35					40					45
His	Met	Asp	Pro	Asn	Tyr	Cys	His	Pro	Ser	Thr	Ser	Leu	His	Leu
				50					55					60
Cys	Ser	Leu	Ala	Trp	Ser	Phe	Thr	Arg	Leu	Leu	His	Pro	Pro	Leu
				65					70					75
Ser	Pro	Gly	Ile	Ser	Gln	Val	Val	Lys	Asp	His	Val	Thr	Lys	Pro
				80					85					90
Thr	Ala	Met	Ala	Gln	Gly	Arg	Val	Ala	His	Leu	Ile	Glu	Trp	Lys
				95					100					105
Gly	Trp	Ser	Lys	Pro	Ser	Asp	Ser	Pro	Ala	Ala	Leu	Glu	Ser	Ala
				110					115					120

Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala Arg	125	130	135
Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys	140	145	150
Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp	155	160	165
Ser Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala	170	175	180
Gly Gln Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly	185	190	195
His Arg Phe Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu	200	205	210
Ser Asp Cys Ser Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser	215	220	225
Leu Cys Ser Leu Glu Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu	230	235	240
Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro	245	250	255
Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala	260	265	270
Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser	275	280	285
Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu	290	295	300
Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser	305	310	315
Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp Glu Asp Glu Ala	320	325	330
Glu Pro Glu Glu Gln	335		

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<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 34

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<220>
<223> Synthetic oligonucleotide probe

<400> 36
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<210> 37
<211> 23
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 37
ggcgagccct aactatccag gag 23

<210> 38
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<210> 40
<211> 2084

<212> DNA

<213> Homo sapiens

<400> 40

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<210> 41

<211> 334

<212> PRT

<213> Homo sapiens

<400> 41

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Ser	Leu	Leu	Ser	Gly	Ser	His	Gly	Lys	Glu	Asn	Gln	Asp	Ile	Asn
				20					25					30
Thr	Thr	Gln	Asn	Ile	Ala	Glu	Val	Phe	Lys	Thr	Met	Glu	Asn	Lys
				35					40					45
Pro	Ile	Ser	Leu	Glu	Ser	Glu	Ala	Asn	Leu	Asn	Ser	Asp	Lys	Glu
				50					55					60
Asn	Ile	Thr	Thr	Ser	Asn	Leu	Lys	Ala	Ser	His	Ser	Pro	Pro	Leu
				65					70					75
Asn	Leu	Pro	Asn	Asn	Ser	His	Gly	Ile	Thr	Asp	Phe	Ser	Ser	Asn
				80					85					90
Ser	Ser	Ala	Glu	His	Ser	Leu	Gly	Ser	Leu	Lys	Pro	Thr	Ser	Thr
				95					100					105

Ile Ser Thr Ser	Pro Pro Leu Ile His	Ser Phe Val Ser Lys	Val
	110	115	120
Pro Trp Asn Ala	Pro Ile Ala Asp Glu	Asp Leu Leu Pro Ile	Ser
	125	130	135
Ala His Pro Asn	Ala Thr Pro Ala Leu	Ser Ser Glu Asn Phe	Thr
	140	145	150
Trp Ser Leu Val	Asn Asp Thr Val Lys	Thr Pro Asp Asn Ser	Ser
	155	160	165
Ile Thr Val Ser	Ile Leu Ser Ser Glu	Pro Thr Ser Pro Ser	Val
	170	175	180
Thr Pro Leu Ile	Val Glu Pro Ser Gly	Trp Leu Thr Thr Asn	Ser
	185	190	195
Asp Ser Phe Thr	Gly Phe Thr Pro Tyr	Gln Glu Lys Thr Thr	Leu
	200	205	210
Gln Pro Thr Leu	Lys Phe Thr Asn Asn	Ser Lys Leu Phe Pro	Asn
	215	220	225
Thr Ser Asp Pro	Gln Lys Glu Asn Arg	Asn Thr Gly Ile Val	Phe
	230	235	240
Gly Ala Ile Leu	Gly Ala Ile Leu Gly	Val Ser Leu Leu Thr	Leu
	245	250	255
Val Gly Tyr Leu	Leu Cys Gly Lys Arg	Lys Thr Asp Ser Phe	Ser
	260	265	270
His Arg Arg Leu	Tyr Asp Asp Arg Asn	Glu Pro Val Leu Arg	Leu
	275	280	285
Asp Asn Ala Pro	Glu Pro Tyr Asp Val	Ser Phe Gly Asn Ser	Ser
	290	295	300
Tyr Tyr Asn Pro	Thr Leu Asn Asp Ser	Ala Met Pro Glu Ser	Glu
	305	310	315
Glu Asn Ala Arg	Asp Gly Ile Pro Met	Asp Asp Ile Pro Pro	Leu
	320	325	330

Arg Thr Ser Val

<210> 42

<211> 1594

<212> DNA

<213> Homo sapiens

<400> 42

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ccctataata aattttactc tatacaaaaaa aaaaaaaaaa aaaa 1594

<210> 43

<211> 263

<212> PRT

<213> Homo sapiens

<400> 43

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Glu	Ala	Arg	Gln	Asp	Val	Glu	Ala	Leu	Leu	Ser	Arg	Thr	Val	Arg
				20					25					30

Thr	Gln	Ile	Leu	Thr	Gly	Lys	Glu	Leu	Arg	Val	Ala	Thr	Gln	Glu
				35					40					45

Lys	Glu	Gly	Ser	Ser	Gly	Arg	Cys	Met	Leu	Thr	Leu	Leu	Gly	Leu
				50					55					60

Ser	Phe	Ile	Leu	Ala	Gly	Leu	Ile	Val	Gly	Gly	Ala	Cys	Ile	Tyr
				65					70					75

Lys	Tyr	Phe	Met	Pro	Lys	Ser	Thr	Ile	Tyr	Arg	Gly	Glu	Met	Cys
				80					85					90

Phe	Phe	Asp	Ser	Glu	Asp	Pro	Ala	Asn	Ser	Leu	Arg	Gly	Gly	Glu
				95					100					105

Pro	Asn	Phe	Leu	Pro	Val	Thr	Glu	Glu	Ala	Asp	Ile	Arg	Glu	Asp
				110					115					120

Asp	Asn	Ile	Ala	Ile	Ile	Asp	Val	Pro	Val	Pro	Ser	Phe	Ser	Asp
				125					130					135

Ser	Asp	Pro	Ala	Ala	Ile	Ile	His	Asp	Phe	Glu	Lys	Gly	Met	Thr
				140					145					150

Ala	Tyr	Leu	Asp	Leu	Leu	Leu	Gly	Asn	Cys	Tyr	Leu	Met	Pro	Leu
				155					160					165

Asn	Thr	Ser	Ile	Val	Met	Pro	Pro	Lys	Asn	Leu	Val	Glu	Leu	Phe
				170					175					180

Gly	Lys	Leu	Ala	Ser	Gly	Arg	Tyr	Leu	Pro	Gln	Thr	Tyr	Val	Val
				185					190					195

Arg	Glu	Asp	Leu	Val	Ala	Val	Glu	Glu	Ile	Arg	Asp	Val	Ser	Asn
				200					205					210

Leu	Gly	Ile	Phe	Ile	Tyr	Gln	Leu	Cys	Asn	Asn	Arg	Lys	Ser	Phe
				215					220					225

Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala

	230	235	240
Ile Asp Lys Cys Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile			
	245	250	255
Val Glu Thr Lys Ile Cys Gln Glu			
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<210> 45
 <211> 20
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<220>
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<400> 45
 gggaactgct atctgatgcc 20

<210> 46
 <211> 26
 <212> DNA
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<220>
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<400> 46
 caggatctcc tcttgcatgc tgcagc 26

<210> 47
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<400> 47
 cttctcgaac cacataagtt tgaggcag 28

<210> 48
 <211> 25
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 <213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 48

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<210> 49

<211> 1969

<212> DNA

<213> Homo sapiens

<400> 49

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<210> 50

<211> 283

<212> PRT

<213> Homo sapiens

<400> 50

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				20				25					30	
Lys	Ala	Thr	Phe	Leu	Glu	Asp	Val	Ala	Gly	Ser	Gly	Glu	Ala	Glu
				35				40					45	
Gly	Ser	Ser	Ala	Ser	Ser	Pro	Ser	Leu	Pro	Pro	Pro	Trp	Thr	Pro
				50				55					60	
Ala	Leu	Ser	Pro	Thr	Ser	Met	Gly	Pro	Gln	Pro	Thr	Thr	Leu	Gly
				65				70					75	
Gly	Pro	Ser	Pro	Pro	Thr	Asn	Phe	Leu	Asp	Gly	Ile	Val	Asp	Phe

80					85					90				
Phe	Arg	Gln	Tyr	Val	Met	Leu	Ile	Ala	Val	Val	Gly	Ser	Leu	Ala
				95					100					105
Phe	Leu	Leu	Met	Phe	Ile	Val	Cys	Ala	Ala	Val	Ile	Thr	Arg	Gln
				110					115					120
Lys	Gln	Lys	Ala	Ser	Ala	Tyr	Tyr	Pro	Ser	Ser	Phe	Pro	Lys	Lys
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Lys	Tyr	Val	Asp	Gln	Ser	Asp	Arg	Ala	Gly	Gly	Pro	Arg	Ala	Phe
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Ser	Glu	Val	Pro	Asp	Arg	Ala	Pro	Asp	Ser	Arg	Pro	Glu	Glu	Ala
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Leu	Asp	Ser	Ser	Arg	Gln	Leu	Gln	Ala	Asp	Ile	Leu	Ala	Ala	Thr
				170					175					180
Gln	Asn	Leu	Lys	Ser	Pro	Thr	Arg	Ala	Ala	Leu	Gly	Gly	Gly	Asp
				185					190					195
Gly	Ala	Arg	Met	Val	Glu	Gly	Arg	Gly	Ala	Glu	Glu	Glu	Glu	Lys
				200					205					210
Gly	Ser	Gln	Glu	Gly	Asp	Gln	Glu	Val	Gln	Gly	His	Gly	Val	Pro
				215					220					225
Val	Glu	Thr	Pro	Glu	Ala	Gln	Glu	Glu	Pro	Cys	Ser	Gly	Val	Leu
				230					235					240
Glu	Gly	Ala	Val	Val	Ala	Gly	Glu	Gly	Gln	Gly	Glu	Leu	Glu	Gly
				245					250					255
Ser	Leu	Leu	Leu	Ala	Gln	Glu	Ala	Gln	Gly	Pro	Val	Gly	Pro	Pro
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Glu	Ser	Pro	Cys	Ala	Cys	Ser	Ser	Val	His	Pro	Ser	Val		
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 <212> DNA
 <213> Homo sapiens

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<211> 440

<212> PRT

<213> Homo sapiens

<400> 52

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Thr	Gly	Thr	Asn	Ile	Gly	Glu	Ala	Leu	Gly	His	Gly	Leu	Gly	Asp
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Ala	Leu	Ser	Glu	Gly	Val	Gly	Lys	Ala	Ile	Gly	Lys	Glu	Ala	Gly
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Gly	Ala	Ala	Gly	Ser	Lys	Val	Ser	Glu	Ala	Leu	Gly	Gln	Gly	Thr
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Arg	Glu	Ala	Val	Gly	Thr	Gly	Val	Arg	Gln	Val	Pro	Gly	Phe	Gly
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Ala	Ala	Asp	Ala	Leu	Gly	Asn	Arg	Val	Gly	Glu	Ala	Ala	His	Ala
				95					100					105

Leu	Gly	Asn	Thr	Gly	His	Glu	Ile	Gly	Arg	Gln	Ala	Glu	Asp	Val
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Ile	Arg	His	Gly	Ala	Asp	Ala	Val	Arg	Gly	Ser	Trp	Gln	Gly	Val
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Pro	Gly	His	Ser	Gly	Ala	Trp	Glu	Thr	Ser	Gly	Gly	His	Gly	Ile
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Phe	Gly	Ser	Gln	Gly	Gly	Leu	Gly	Gly	Gln	Gly	Gln	Gly	Asn	Pro
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Gly	Gly	Asn	Gly	Gly	Pro	Pro	Asn	Phe	Gly	Thr	Asn	Thr	Gln	Gly
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Ala	Val	Ala	Gln	Pro	Gly	Tyr	Gly	Ser	Val	Arg	Ala	Ser	Asn	Gln
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Asn	Glu	Gly	Cys	Thr	Asn	Pro	Pro	Pro	Ser	Gly	Ser	Gly	Gly	Gly
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Ser	Ser	Asn	Ser	Gly	Gly	Gly	Ser	Gly	Ser	Gln	Ser	Gly	Ser	Ser	245	250	255
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Gly	Ser	Ser	Ser	Gly	Ser	Ser	Ser	Gly	Ser	Ser	Ser	Gly	Gly	Ser	275	280	285
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Lys	Pro	Gly	Cys	Glu	Lys	Pro	Gly	Asn	Glu	Ala	Arg	Gly	Ser	Gly	335	340	345
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Pro	Gly	Met	Phe	Asn	Phe	Asp	Thr	Phe	Trp	Lys	Asn	Phe	Lys	Ser	410	415	420
Lys	Leu	Gly	Phe	Ile	Asn	Trp	Asp	Ala	Ile	Asn	Lys	Asp	Gln	Arg	425	430	435
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<212> DNA

<213> Homo sapiens

<400> 53

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<212> PRT
<213> Homo sapiens

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His Gly Leu Asp Asn Ala Pro Val Val Asp Gln Gln Leu Leu Tyr
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Thr Cys Cys Pro Tyr Ile Gly Glu Leu Arg Lys Leu Leu Ala Ser
65 70 75
Trp Val Ser Gly Ser Ser Gly Arg Ser Gly Gly Phe Met Arg Lys
80 85 90
Ile Thr Pro Thr Thr Thr Thr Ser Leu Gly Ala Gln Pro Ser Gln
95 100 105
Thr Ser Gln Gly Leu Gln Ala Gln Leu Ala Gln Ala Phe Phe His
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Asn Gln Pro Pro Ser Leu Arg Arg Thr Val Glu Phe Val Ala Glu
125 130 135
Arg Ile Gly Ser Asn Cys Val Lys His Ile Lys Ala Thr Leu Val
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Val	Thr	Gln	Gly	Glu	Glu	Gly	Gly	Asp	Pro	Ala	Gln	Leu	Leu	Glu	
				170					175					180	
Ile	Leu	Cys	Ser	Gln	Leu	Cys	Pro	His	Gly	Ala	Gln	Ala	Leu	Ala	
				185					190					195	
Leu	Gly	Arg	Glu	Phe	Cys	Gln	Arg	Lys	Ser	Pro	Gly	Ala	Val	Arg	
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Ala	Leu	Leu	Pro	Glu	Glu	Thr	Pro	Ala	Ala	Val	Leu	Ser	Ser	Ala	
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Glu	Asn	Ile	Ala	Val	Gly	Leu	Ala	Thr	Glu	Lys	Ala	Cys	Ala	Trp	
				230					235					240	
Leu	Ser	Ala	Asn	Ile	Thr	Ala	Leu	Ile	Arg	Arg	Glu	Val	Lys	Ala	
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Ala	Val	Ser	Arg	Thr	Leu	Arg	Ala	Gln	Gly	Pro	Glu	Pro	Ala	Ala	
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Arg	Gly	Glu	Arg	Arg	Gly	Cys	Ser	Arg	Ala						
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<210> 55

<211> 2401

<212> DNA

<213> Homo sapiens

<400> 55

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<211> 299

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<400> 56

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Pro	Val	Asn	Leu	Lys	Lys	Trp	Ser	Ile	Thr	Asp	Gly	Tyr	Val	Pro
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Ile	Leu	Gly	Asn	Lys	Thr	Leu	Pro	Ser	Arg	Cys	His	Gln	Cys	Val
				65					70					75

Ile	Val	Ser	Ser	Ser	Ser	His	Leu	Leu	Gly	Thr	Lys	Leu	Gly	Pro
				80					85					90

Glu	Ile	Glu	Arg	Ala	Glu	Cys	Thr	Ile	Arg	Met	Asn	Asp	Ala	Pro
				95					100					105

Thr	Thr	Gly	Tyr	Ser	Ala	Asp	Val	Gly	Asn	Lys	Thr	Thr	Tyr	Arg
				110					115					120

Val	Val	Ala	His	Ser	Ser	Val	Phe	Arg	Val	Leu	Arg	Arg	Pro	Gln
				125					130					135

Glu	Phe	Val	Asn	Arg	Thr	Pro	Glu	Thr	Val	Phe	Ile	Phe	Trp	Gly
				140					145					150

Pro	Pro	Ser	Lys	Met	Gln	Lys	Pro	Gln	Gly	Ser	Leu	Val	Arg	Val
				155					160					165

Ile	Gln	Arg	Ala	Gly	Leu	Val	Phe	Pro	Asn	Met	Glu	Ala	Tyr	Ala
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Gly Trp Phe Thr	Met Val Ile Ala Val	Glu Leu Cys Asp His Val			
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His Val Tyr Gly	Met Val Pro Pro Asn	Tyr Cys Ser Gln Arg Pro			
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Asp Glu Cys Val	Thr Tyr Ile Gln Asn	Glu His Ser Arg Lys Gly			
	260		265		270
Asn His His Arg	Phe Ile Thr Glu Lys	Arg Val Phe Ser Ser Trp			
	275		280		285
Ala Gln Leu Tyr	Gly Ile Thr Phe Ser	His Pro Ser Trp Thr			
	290		295		

<210> 57
 <211> 4277
 <212> DNA
 <213> Homo sapiens

<400> 57
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 cagcggaccg ggagcgacgc agcttgaggg aagcatccct agctgttggc 100
 gcagaggggc gaggtgaag ccgagtggcc cgaggtgtct gaggggctgg 150
 ggcaaagggtg aaagagtttc agaacaagct tcttggaacc catgacccat 200
 gaagtcttgt cgacatttat accgtctgag ggtagcagct cgaaactaga 250
 agaagtggag tgttgccagg gacggcagta tctctttgtg tgaccctggc 300
 ggcctatggg acgttggtt cagaccttg tgatacacca tgctgcgtgg 350
 gacgatgacg gcgtggagag gaatgaggcc tgaggtcaca ctggcttgcc 400
 tctcctagc cacagcaggc tgctttgctg acttgaacga ggtccctcag 450
 gtcaccgtcc agcctgcgtc caccgtccag aagcccggag gcactgtgat 500
 cttgggctgc gtggtggaac ctccaaggat gaatgtaacc tggcgctga 550
 atggaaagga gctgaatggc tcggatgatg ctctgggtgt cctcatcacc 600
 cacgggaccc tcgtcatcac tgcccttaac aaccacactg tgggacggta 650

ccagtgtgtg gcccggatgc ctgcgggggc tgtggccagc gtgccagcca 700
ctgtgacact agccaatctc caggacttca agttagatgt gcagcacgtg 750
attgaagtgg atgagggaaa cacagcagtc attgcctgcc acctgcctga 800
gagccacccc aaagcccagg tccggtacag cgtcaaacia gagtggctgg 850
aggcctccag aggttaactac ctgatcatgc cctcagggaa cctccagatt 900
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cccagtgacc caggaagtga aaacctccgg ctccagcgac aggctacgtg 1000
tgcgcgcgtc caccgctgag gctgcccga tcatctacc cccagaggcc 1050
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cagtggaaac ccacccccac gggtcacctg ggccaaggat gggtcagtg 1150
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accaccagcg aggaggactc aggcacctac cgctgcatgg ccgacaatgg 1250
gggtgggcag cccggggcag cggtcatcct ctacaatgtc cagggtgttg 1300
aaccacctga ggtcaccatg gagctatccc agctgggtcat cccctggggc 1350
cagagtgcc a agcttacctg tgagggtcgt gggaaccccc cgcctccgt 1400
gctgtggctg aggaatgctg tgcccctcat ctccagccag cgcctccggc 1450
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accagacttg accccgggag cttgtatgaa gtggagatgg cagcttacia 2000
ctgtgcggga gagggccaga cagccatggt caccttccga actggacggc 2050

ggcccaaacc cgagatcatg gccagcaaag agcagcagat ccagagagac 2100
gaccctggag ccagtcccca gagcagcagc cagccagacc acggccgcct 2150
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cctcagtgtg cgtgacctgg attccccgtg ggaatggtgg gttcccaatc 2250
cagtccttcc gtgtggagta caagaagcta aagaaagtgg gagactggat 2300
tctggccacc agcgccatcc ccccatcgcg gctgtccgtg gagatcacgg 2350
gcctagagaa aggcacctcc tacaagtttc gagtccgggc tctgaacatg 2400
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tcacggatgc ggtcaatgag accaccatca tgctcaagtg gatgtacatc 2550
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accacagac agtgacaatg atagtgacta caagaaggat atggtggaag 2650
gggacaagta ctggcactcc atcagccacc tgcagccaga gacctcctac 2700
gacattaaga tgcagtgcct caatgaagga ggggagagcg agttcagcaa 2750
cgtgatgatc tgtgagacca aagctcgga gtcttctggc cagcctgggc 2800
gactgccacc cccaactctg gccccaccac agccgcccct tectgaaacc 2850
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tcaccttcat ccccttctgc ttgtggaggg cctgggtctaa gcaaaaacat 3000
acaacagacc tgggttttcc tcgaagtgcc ctccaccct cctgcccgtg 3050
tactatggtg ccattgggag gactcccagg ccaccaggcc agtggacagc 3100
cctacctcag tggcatcagt ggacgggcct gtgctaattg gatccacatg 3150
aataggggct gcccctcggc tgcagtgggc taccggggca tgaagcccca 3200
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tgaggcagac ccatcttggc aatggatatg acccccaaag tcaccagatc 3300
acgaggggtc ccaagtctag cccggacgag ggctctttct tatacacact 3350
gcccgcagc tccactcacc agctgctgca gcccatac gactgctgcc 3400
aacgccagga gcagcctgct gctgtgggcc agtcaggggt gaggagagcc 3450
cccgcagtc ctgtcctgga agcagtgtgg gaccctccat ttcactcagg 3500

gcccccatgc tgcttgggcc ttgtgccagt tgaagaggtg gacagtcctg 3550
 actcctgcc aagttagtga ggagactggt gtccccagca cccgtaggg 3600
 gcctacgtag gacaggaacc tggaatgcag ctctccccgg ggccactggt 3650
 gcgtgtgtct ttgaaacac cacctctcac aatttaggca gaagctgata 3700
 tcccagaaag actatatatt gttttttttt taaaaaaaaa agaagaaaaa 3750
 agagacagag aaaattggta ttattttttc tattatagcc atatttatat 3800
 atttatgcac ttgtaaataa atgtatatgt ttataattc tggagagaca 3850
 taaggagtcc taccggttga ggttggagag ggaaaataaa gaagctgcc 3900
 cctaacagga gtcaccagg aaagcaccgc acaggctggc gcgggacaga 3950
 ctctaacct ggggcctctg cagtggcagg cgaggctgca ggaggccac 4000
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 atggctggat ccggtgctac gggaaacatt ttcctaagat gcccatgaga 4150
 acagaccaag atgtgtacag cactatgagc attaaaaaac cttccagaat 4200
 caataatccg tggcaacata tctctgtaaa aacaaacact gtaacttcta 4250
 aataaatgtt tagtcttccc tgtaaaa 4277

<210> 58
 <211> 1115
 <212> PRT
 <213> Homo sapiens

<400> 58
 Met Leu Arg Gly Thr Met Thr Ala Trp Arg Gly Met Arg Pro Glu
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 Val Thr Leu Ala Cys Leu Leu Leu Ala Thr Ala Gly Cys Phe Ala
 20 25 30
 Asp Leu Asn Glu Val Pro Gln Val Thr Val Gln Pro Ala Ser Thr
 35 40 45
 Val Gln Lys Pro Gly Gly Thr Val Ile Leu Gly Cys Val Val Glu
 50 55 60
 Pro Pro Arg Met Asn Val Thr Trp Arg Leu Asn Gly Lys Glu Leu
 65 70 75
 Asn Gly Ser Asp Asp Ala Leu Gly Val Leu Ile Thr His Gly Thr
 80 85 90

Leu Val Ile Thr	Ala	Leu Asn Asn His	Thr Val Gly Arg Tyr	Gln
	95		100	105
Cys Val Ala Arg	Met	Pro Ala Gly Ala	Val Ala Ser Val Pro	Ala
	110		115	120
Thr Val Thr Leu	Ala Asn Leu Gln Asp	Phe Lys Leu Asp	Val	Gln
	125		130	135
His Val Ile Glu	Val Asp Glu Gly Asn	Thr Ala Val Ile	Ala	Cys
	140		145	150
His Leu Pro Glu	Ser His Pro Lys Ala	Gln Val Arg Tyr	Ser	Val
	155		160	165
Lys Gln Glu Trp	Leu Glu Ala Ser Arg	Gly Asn Tyr Leu	Ile	Met
	170		175	180
Pro Ser Gly Asn	Leu Gln Ile Val Asn	Ala Ser Gln Glu Asp	Glu	
	185		190	195
Gly Met Tyr Lys	Cys Ala Ala Tyr Asn	Pro Val Thr Gln Glu	Val	
	200		205	210
Lys Thr Ser Gly	Ser Ser Asp Arg Leu	Arg Val Arg Arg	Ser	Thr
	215		220	225
Ala Glu Ala Ala	Arg Ile Ile Tyr Pro	Pro Glu Ala Gln Thr	Ile	
	230		235	240
Ile Val Thr Lys	Gly Gln Ser Leu Ile	Leu Glu Cys Val Ala	Ser	
	245		250	255
Gly Ile Pro Pro	Pro Arg Val Thr Trp	Ala Lys Asp Gly Ser	Ser	
	260		265	270
Val Thr Gly Tyr	Asn Lys Thr Arg Phe	Leu Leu Ser Asn Leu	Leu	
	275		280	285
Ile Asp Thr Thr	Ser Glu Glu Asp Ser	Gly Thr Tyr Arg Cys	Met	
	290		295	300
Ala Asp Asn Gly	Val Gly Gln Pro Gly	Ala Ala Val Ile Leu	Tyr	
	305		310	315
Asn Val Gln Val	Phe Glu Pro Pro Glu	Val Thr Met Glu Leu	Ser	
	320		325	330
Gln Leu Val Ile	Pro Trp Gly Gln Ser	Ala Lys Leu Thr Cys	Glu	
	335		340	345
Val Arg Gly Asn	Pro Pro Pro Ser Val	Leu Trp Leu Arg Asn	Ala	
	350		355	360
Val Pro Leu Ile	Ser Ser Gln Arg Leu	Arg Leu Ser Arg Arg	Ala	
	365		370	375

Leu Arg Val Leu Ser Met Gly Pro Glu Asp Glu Gly Val Tyr Gln	380	385	390
Cys Met Ala Glu Asn Glu Val Gly Ser Ala His Ala Val Val Gln	395	400	405
Leu Arg Thr Ser Arg Pro Ser Ile Thr Pro Arg Leu Trp Gln Asp	410	415	420
Ala Glu Leu Ala Thr Gly Thr Pro Pro Val Ser Pro Ser Lys Leu	425	430	435
Gly Asn Pro Glu Gln Met Leu Arg Gly Gln Pro Ala Leu Pro Arg	440	445	450
Pro Pro Thr Ser Val Gly Pro Ala Ser Pro Lys Cys Pro Gly Glu	455	460	465
Lys Gly Gln Gly Ala Pro Ala Glu Ala Pro Ile Ile Leu Ser Ser	470	475	480
Pro Arg Thr Ser Lys Thr Asp Ser Tyr Glu Leu Val Trp Arg Pro	485	490	495
Arg His Glu Gly Ser Gly Arg Ala Pro Ile Leu Tyr Tyr Val Val	500	505	510
Lys His Arg Lys Gln Val Thr Asn Ser Ser Asp Asp Trp Thr Ile	515	520	525
Ser Gly Ile Pro Ala Asn Gln His Arg Leu Thr Leu Thr Arg Leu	530	535	540
Asp Pro Gly Ser Leu Tyr Glu Val Glu Met Ala Ala Tyr Asn Cys	545	550	555
Ala Gly Glu Gly Gln Thr Ala Met Val Thr Phe Arg Thr Gly Arg	560	565	570
Arg Pro Lys Pro Glu Ile Met Ala Ser Lys Glu Gln Gln Ile Gln	575	580	585
Arg Asp Asp Pro Gly Ala Ser Pro Gln Ser Ser Ser Gln Pro Asp	590	595	600
His Gly Arg Leu Ser Pro Pro Glu Ala Pro Asp Arg Pro Thr Ile	605	610	615
Ser Thr Ala Ser Glu Thr Ser Val Tyr Val Thr Trp Ile Pro Arg	620	625	630
Gly Asn Gly Gly Phe Pro Ile Gln Ser Phe Arg Val Glu Tyr Lys	635	640	645
Lys Leu Lys Lys Val Gly Asp Trp Ile Leu Ala Thr Ser Ala Ile	650	655	660

Pro	Pro	Ser	Arg	Leu	Ser	Val	Glu	Ile	Thr	Gly	Leu	Glu	Lys	Gly	
				665						670				675	
Thr	Ser	Tyr	Lys	Phe	Arg	Val	Arg	Ala	Leu	Asn	Met	Leu	Gly	Glu	
				680						685				690	
Ser	Glu	Pro	Ser	Ala	Pro	Ser	Arg	Pro	Tyr	Val	Val	Ser	Gly	Tyr	
				695						700				705	
Ser	Gly	Arg	Val	Tyr	Glu	Arg	Pro	Val	Ala	Gly	Pro	Tyr	Ile	Thr	
				710						715				720	
Phe	Thr	Asp	Ala	Val	Asn	Glu	Thr	Thr	Ile	Met	Leu	Lys	Trp	Met	
				725						730				735	
Tyr	Ile	Pro	Ala	Ser	Asn	Asn	Asn	Thr	Pro	Ile	His	Gly	Phe	Tyr	
				740						745				750	
Ile	Tyr	Tyr	Arg	Pro	Thr	Asp	Ser	Asp	Asn	Asp	Ser	Asp	Tyr	Lys	
				755						760				765	
Lys	Asp	Met	Val	Glu	Gly	Asp	Lys	Tyr	Trp	His	Ser	Ile	Ser	His	
				770						775				780	
Leu	Gln	Pro	Glu	Thr	Ser	Tyr	Asp	Ile	Lys	Met	Gln	Cys	Phe	Asn	
				785						790				795	
Glu	Gly	Gly	Glu	Ser	Glu	Phe	Ser	Asn	Val	Met	Ile	Cys	Glu	Thr	
				800						805				810	
Lys	Ala	Arg	Lys	Ser	Ser	Gly	Gln	Pro	Gly	Arg	Leu	Pro	Pro	Pro	
				815						820				825	
Thr	Leu	Ala	Pro	Pro	Gln	Pro	Pro	Leu	Pro	Glu	Thr	Ile	Glu	Arg	
				830						835				840	
Pro	Val	Gly	Thr	Gly	Ala	Met	Val	Ala	Arg	Ser	Ser	Asp	Leu	Pro	
				845						850				855	
Tyr	Leu	Ile	Val	Gly	Val	Val	Leu	Gly	Ser	Ile	Val	Leu	Ile	Ile	
				860						865				870	
Val	Thr	Phe	Ile	Pro	Phe	Cys	Leu	Trp	Arg	Ala	Trp	Ser	Lys	Gln	
				875						880				885	
Lys	His	Thr	Thr	Asp	Leu	Gly	Phe	Pro	Arg	Ser	Ala	Leu	Pro	Pro	
				890						895				900	
Ser	Cys	Pro	Tyr	Thr	Met	Val	Pro	Leu	Gly	Gly	Leu	Pro	Gly	His	
				905						910				915	
Gln	Ala	Ser	Gly	Gln	Pro	Tyr	Leu	Ser	Gly	Ile	Ser	Gly	Arg	Ala	
				920						925				930	
Cys	Ala	Asn	Gly	Ile	His	Met	Asn	Arg	Gly	Cys	Pro	Ser	Ala	Ala	
				935						940				945	

Val Gly Tyr Pro Gly Met Lys Pro Gln Gln His Cys Pro Gly Glu	950	955	960
Leu Gln Gln Gln Ser Asp Thr Ser Ser Leu Leu Arg Gln Thr His	965	970	975
Leu Gly Asn Gly Tyr Asp Pro Gln Ser His Gln Ile Thr Arg Gly	980	985	990
Pro Lys Ser Ser Pro Asp Glu Gly Ser Phe Leu Tyr Thr Leu Pro	995	1000	1005
Asp Asp Ser Thr His Gln Leu Leu Gln Pro His His Asp Cys Cys	1010	1015	1020
Gln Arg Gln Glu Gln Pro Ala Ala Val Gly Gln Ser Gly Val Arg	1025	1030	1035
Arg Ala Pro Asp Ser Pro Val Leu Glu Ala Val Trp Asp Pro Pro	1040	1045	1050
Phe His Ser Gly Pro Pro Cys Cys Leu Gly Leu Val Pro Val Glu	1055	1060	1065
Glu Val Asp Ser Pro Asp Ser Cys Gln Val Ser Gly Gly Asp Trp	1070	1075	1080
Cys Pro Gln His Pro Val Gly Ala Tyr Val Gly Gln Glu Pro Gly	1085	1090	1095
Met Gln Leu Ser Pro Gly Pro Leu Val Arg Val Ser Phe Glu Thr	1100	1105	1110
Pro Pro Leu Thr Ile	1115		

<210> 59

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 59

gggaaacaca gcagtcattg cctgc 25

<210> 60

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 60

gcacacgtag cctgtcgctg gagc 24

<210> 61
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 61
caccoccaaag cccaggtccg gtacagcgtc aaacaagagt gg 42

<210> 62
<211> 1661
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 678
<223> unknown base

<400> 62
cgaggagctg ggtcgtcatg atccggaccc cattgtcggc ctctgcccat 50
cgctgtctcc tcccaggctc ccgcggccga ccccgcgca acatgcagcc 100
cacgggcccgc gagggttccc gcgcgtcag ccggcggtat ctgcggcgtc 150
tgctgtcct gctactgtg ctgtgtgtgc ggcagcccgt aacccgcgcg 200
gagaccacgc cgggcgcccc cagagccctc tccacgttg gctccccag 250
cctcttcacc acgcgggtg tcccagcgc cctcactacc ccaggcctca 300
ctacgccagg ccccccaaa accctggacc ttcggggctc gcgcaggcc 350
ctgatgcgga gtttcccact cgtggacggc cacaatgacc tgccccaggt 400
cctgagacag cgttacaaga atgtgcttca ggatgttaac ctgcgaaatt 450
tcagccatgg tcagaccagc ctggacaggc ttagagacgg cctcgtgggt 500
gccagttct ggtcagcctc cgtctcatgc cagtcccagg accagactgc 550
cgtgcgcctc gccctggagc agattgacct cattcaccgc atgtgtgcct 600
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caaaagctgg cctgcctcat tggcgtgnag ggtggtcact cactggacag 700
cagcctctct gtgtgcgca gtttctatgt gctgggggtg cgctacctga 750
cacttacctt cacctgcagt acaccatggg cagagagttc caccaagttc 800
agacaccaca tgtacaccaa cgtcagcggg ttgacaagct ttggtgagaa 850

agtagtagag gagttgaacc gcctgggcat gatgatagat ttgtcctatg 900
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 gccaaccaat cgggtcccct ggaggctctc aaatgcctcc ccataccttg 1500
 ttccaggcct tgtggctgct gccaccatcc caaccttcac ccagtggctc 1550
 tgctgacaca gtcgggtccc gcagaggtca ctgtggcaaa gcctcacaaa 1600
 gccccctctc ctagttcatt cacaagcata tgctgagaat aaacatgtta 1650
 cacatggaaa a 1661

<210> 63
 <211> 487
 <212> PRT
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 196, 386
 <223> unknown amino acid

<400> 63
 Met Gln Pro Thr Gly Arg Glu Gly Ser Arg Ala Leu Ser Arg Arg
 1 5 10 15
 Tyr Leu Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Leu Arg
 20 25 30
 Gln Pro Val Thr Arg Ala Glu Thr Thr Pro Gly Ala Pro Arg Ala
 35 40 45
 Leu Ser Thr Leu Gly Ser Pro Ser Leu Phe Thr Thr Pro Gly Val
 50 55 60

Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro			
				65					70					75			
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser			
				80					85					90			
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg			
				95					100					105			
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe			
				110					115					120			
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val			
				125					130					135			
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp			
				140					145					150			
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His			
				155					160					165			
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala			
				170					175					180			
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val			
				185					190					195			
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser			
				200					205					210			
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys			
				215					220					225			
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met			
				230					235					240			
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val			
				245					250					255			
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala			
				260					265					270			
Ser	Asp	Thr	Leu	Ile	Arg	Arg	Val	Leu	Glu	Val	Ser	Gln	Ala	Pro			
				275					280					285			
Val	Ile	Phe	Ser	His	Ser	Ala	Ala	Arg	Ala	Val	Cys	Asp	Asn	Leu			
				290					295					300			
Leu	Asn	Val	Pro	Asp	Asp	Ile	Leu	Gln	Leu	Leu	Lys	Asn	Gly	Gly			
				305					310					315			
Ile	Val	Met	Val	Thr	Leu	Ser	Met	Gly	Val	Leu	Gln	Cys	Asn	Leu			
				320					325					330			
Leu	Ala	Asn	Val	Ser	Thr	Val	Ala	Asp	His	Phe	Asp	His	Ile	Arg			
				335					340					345			

Ala Val Ile Gly	Ser Glu Phe Ile Gly	Ile Gly Gly Asn Tyr Asp	350	355	360
Gly Thr Gly Arg	Phe Pro Gln Gly Leu	Glu Asp Val Ser Thr Tyr	365	370	375
Pro Val Leu Ile	Glu Glu Leu Leu Ser	Arg Xaa Trp Ser Glu Glu	380	385	390
Glu Leu Gln Gly	Val Leu Arg Gly Asn	Leu Leu Arg Val Phe Arg	395	400	405
Gln Val Glu Lys	Val Arg Glu Glu Ser	Arg Ala Gln Ser Pro Val	410	415	420
Glu Ala Glu Phe	Pro Tyr Gly Gln Leu	Ser Thr Ser Cys His Ser	425	430	435
His Leu Val Pro	Gln Asn Gly His Gln	Ala Thr His Leu Glu Val	440	445	450
Thr Lys Gln Pro	Thr Asn Arg Val Pro	Trp Arg Ser Ser Asn Ala	455	460	465
Ser Pro Tyr Leu	Val Pro Gly Leu Val	Ala Ala Ala Thr Ile Pro	470	475	480
Thr Phe Thr Gln	Trp Leu Cys		485		

<210> 64
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 64
 ccttcacctg cagtacacca tgggc 25

<210> 65
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 65
 gtcacacaca gctctggcag ctgag 25

<210> 66
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 66

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<210> 67

<211> 1564

<212> DNA

<213> Homo sapiens

<400> 67

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ggcccagcaa gcctgataag catgaagctc ttatctttgg tggctgtggt 150
cgggtgtttg ctggtgcccc cagctgaagc caacaagagt tctgaagata 200
tccggtgcaa atgcatctgt ccaccttata gaaacatcag tgggcacatt 250
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<210> 68

<211> 183

<212> PRT

<213> Homo sapiens

<400> 68

Met	Lys	Leu	Leu	Ser	Leu	Val	Ala	Val	Val	Gly	Cys	Leu	Leu	Val
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Pro	Pro	Ala	Glu	Ala	Asn	Lys	Ser	Ser	Glu	Asp	Ile	Arg	Cys	Lys
				20					25					30

Cys	Ile	Cys	Pro	Pro	Tyr	Arg	Asn	Ile	Ser	Gly	His	Ile	Tyr	Asn
				35					40					45

Gln	Asn	Val	Ser	Gln	Lys	Asp	Cys	Asn	Cys	Leu	His	Val	Val	Glu
				50					55					60

Pro	Met	Pro	Val	Pro	Gly	His	Asp	Val	Glu	Ala	Tyr	Cys	Leu	Leu
				65					70					75

Cys	Glu	Cys	Arg	Tyr	Glu	Glu	Arg	Ser	Thr	Thr	Thr	Ile	Lys	Val
				80					85					90

Ile	Ile	Val	Ile	Tyr	Leu	Ser	Val	Val	Gly	Ala	Leu	Leu	Leu	Tyr
				95					100					105

Met	Ala	Phe	Leu	Met	Leu	Val	Asp	Pro	Leu	Ile	Arg	Lys	Pro	Asp
				110					115					120

Ala	Tyr	Thr	Glu	Gln	Leu	His	Asn	Glu	Glu	Glu	Asn	Glu	Asp	Ala
				125					130					135

Arg	Ser	Met	Ala	Ala	Ala	Ala	Ala	Ser	Leu	Gly	Gly	Pro	Arg	Ala
				140					145					150

Asn	Thr	Val	Leu	Glu	Arg	Val	Glu	Gly	Ala	Gln	Gln	Arg	Trp	Lys
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Met Leu Ser

<210> 69

<211> 3170

<212> DNA

<213> Homo sapiens

<400> 69

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gcagaatata tttgcagcta ttgactttgt aatttaggaa aaatgtataa 3100
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<210> 70
<211> 259
<212> PRT
<213> Homo sapiens

<400> 70
Met Ala Ala Leu Met Arg Ser Lys Asp Ser Ser Cys Cys Leu Leu
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Leu Leu Ala Ala Val Leu Met Val Glu Ser Ser Gln Ile Gly Ser
20 25 30
Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly Glu
35 40 45
Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly
50 55 60
Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala
65 70 75
Tyr Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys
80 85 90
His Ser Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg
95 100 105
Lys Lys Lys Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr
110 115 120

Arg Cys Asn Asn Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu	125	130	135
Thr Pro His Ile Pro Ala Leu Asp Gly Thr Arg His Arg Asp Arg	140	145	150
Asn His Gly His Tyr Ser Asn His Asp Leu Gly Trp Gln Asn Leu	155	160	165
Gly Arg Pro His Thr Lys Met Ser His Ile Lys Gly His Glu Gly	170	175	180
Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly Phe Cys Cys	185	190	195
Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu His Gln	200	205	210
Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly Leu	215	220	225
Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys	230	235	240
Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val	245	250	255

Cys Gln Lys Ile

<210> 71
 <211> 1809
 <212> DNA
 <213> Homo sapiens

<400> 71
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<210> 72

<211> 363

<212> PRT

<213> Homo sapiens

<400> 72

Met	Cys	Phe	Lys	Ala	Leu	Gly	Arg	Asn	Ser	Val	Leu	Leu	Arg	Ile
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Cys	Ser	Phe	Ile	Pro	Leu	Leu	Lys	Ser	Ser	Val	Leu	Gly	Ser	Gly
				20					25					30
Phe	Gly	Glu	Leu	Ala	Pro	Pro	Lys	Met	Ala	Asn	Ile	Thr	Ser	Ser
				35					40					45
Gln	Ile	Leu	Asp	Gln	Leu	Lys	Ala	Pro	Ser	Leu	Gly	Gln	Phe	Thr
				50					55					60
Thr	Thr	Pro	Ser	Thr	Gln	Gln	Asn	Ser	Thr	Ser	His	Pro	Thr	Thr
				65					70					75
Thr	Thr	Ser	Trp	Asp	Leu	Lys	Pro	Pro	Thr	Ser	Gln	Ser	Ser	Val
				80					85					90
Leu	Ser	His	Leu	Asp	Phe	Lys	Ser	Gln	Pro	Glu	Pro	Ser	Pro	Val
				95					100					105
Leu	Ser	Gln	Leu	Ser	Gln	Arg	Gln	Gln	His	Gln	Ser	Gln	Ala	Val
				110					115					120
Thr	Val	Pro	Pro	Pro	Gly	Leu	Glu	Ser	Phe	Pro	Ser	Gln	Ala	Lys
				125					130					135
Leu	Arg	Glu	Ser	Thr	Pro	Gly	Asp	Ser	Pro	Ser	Thr	Val	Asn	Lys
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Leu	Leu	Gln	Leu	Pro	Ser	Thr	Thr	Ile	Glu	Asn	Ile	Ser	Val	Ser
				155					160					165
Val	His	Gln	Pro	Gln	Pro	Lys	His	Ile	Lys	Leu	Ala	Lys	Arg	Arg
				170					175					180
Ile	Pro	Pro	Ala	Ser	Lys	Ile	Pro	Ala	Ser	Ala	Val	Glu	Met	Pro
				185					190					195
Gly	Ser	Ala	Asp	Val	Thr	Gly	Leu	Asn	Val	Gln	Phe	Gly	Ala	Leu
				200					205					210
Glu	Phe	Gly	Ser	Glu	Pro	Ser	Leu	Ser	Glu	Phe	Gly	Ser	Ala	Pro
				215					220					225
Ser	Ser	Glu	Asn	Ser	Asn	Gln	Ile	Pro	Ile	Ser	Leu	Tyr	Ser	Lys
				230					235					240
Ser	Leu	Ser	Glu	Pro	Leu	Asn	Thr	Ser	Leu	Ser	Met	Thr	Ser	Ala
				245					250					255
Val	Gln	Asn	Ser	Thr	Tyr	Thr	Thr	Ser	Val	Ile	Thr	Ser	Cys	Ser
				260					265					270
Leu	Thr	Ser	Ser	Ser	Leu	Asn	Ser	Ala	Ser	Pro	Val	Ala	Met	Ser

	275	280	285
Ser Ser Tyr Asp Gln Ser Ser Val His Asn Arg Ile Pro Tyr Gln			
	290	295	300
Ser Pro Val Ser Ser Ser Glu Ser Ala Pro Gly Thr Ile Met Asn			
	305	310	315
Gly His Gly Gly Gly Arg Ser Gln Gln Thr Leu Asp Ser Lys Tyr			
	320	325	330
Ser Ser Lys Leu Leu Leu Ser Trp Leu Val Pro Thr Lys Gln Arg			
	335	340	345
Lys Arg Ile Ala His Val Met Trp Lys Thr Pro Val Gly Gln Trp			
	350	355	360

Leu Ile Arg

<210> 73
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 73
 aattcatggc aaatatttcc cttccc 26

<210> 74
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 74
 tggtaaactg gcccaaactc gg 22

<210> 75
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 75
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<210> 76
 <211> 1989
 <212> DNA
 <213> Homo sapiens

<400> 76

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caataaagtc cccatctgat ttttaaaaaa aaaaaaaaaa 1989

<210> 77
<211> 341
<212> PRT
<213> Homo sapiens

<400> 77
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Gln Ser Ser Ala Val Leu Leu His Ser Ala Val Glu Glu Thr Asp
20 25 30
Ala Gly Leu Tyr Thr Cys Asn Leu His His His Tyr Cys His Leu
35 40 45
Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro Pro
50 55 60
Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val
65 70 75
Ala Arg Gly Ala Pro Ala Leu Leu Thr Cys Val Asn Arg Gly His
80 85 90
Val Trp Thr Asp Arg His Val Glu Glu Ala Gln Gln Val Val His
95 100 105
Trp Asp Arg Gln Pro Pro Gly Val Pro His Asp Arg Ala Asp Arg
110 115 120
Leu Leu Asp Leu Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly Pro
125 130 135

Leu	Phe	Leu	Arg	Asp	Arg	Val	Ala	Val	Gly	Ala	Asp	Ala	Phe	Glu	
				140					145					150	
Arg	Gly	Asp	Phe	Ser	Leu	Arg	Ile	Glu	Pro	Leu	Glu	Val	Ala	Asp	
				155					160					165	
Glu	Gly	Thr	Tyr	Ser	Cys	His	Leu	His	His	His	Tyr	Cys	Gly	Leu	
				170					175					180	
His	Glu	Arg	Arg	Val	Phe	His	Leu	Thr	Val	Ala	Glu	Pro	His	Ala	
				185					190					195	
Glu	Pro	Pro	Pro	Arg	Gly	Ser	Pro	Gly	Asn	Gly	Ser	Ser	His	Ser	
				200					205					210	
Gly	Ala	Pro	Gly	Pro	Asp	Pro	Thr	Leu	Ala	Arg	Gly	His	Asn	Val	
				215					220					225	
Ile	Asn	Val	Ile	Val	Pro	Glu	Ser	Arg	Ala	His	Phe	Phe	Gln	Gln	
				230					235					240	
Leu	Gly	Tyr	Val	Leu	Ala	Thr	Leu	Leu	Leu	Phe	Ile	Leu	Leu	Leu	
				245					250					255	
Val	Thr	Val	Leu	Leu	Ala	Ala	Arg	Arg	Arg	Arg	Gly	Gly	Tyr	Glu	
				260					265					270	
Tyr	Ser	Asp	Gln	Lys	Ser	Gly	Lys	Ser	Lys	Gly	Lys	Asp	Val	Asn	
				275					280					285	
Leu	Ala	Glu	Phe	Ala	Val	Ala	Ala	Gly	Asp	Gln	Met	Leu	Tyr	Arg	
				290					295					300	
Ser	Glu	Asp	Ile	Gln	Leu	Asp	Tyr	Lys	Asn	Asn	Ile	Leu	Lys	Glu	
				305					310					315	
Arg	Ala	Glu	Leu	Ala	His	Ser	Pro	Leu	Pro	Ala	Lys	Tyr	Ile	Asp	
				320					325					330	
Leu	Asp	Lys	Gly	Phe	Arg	Lys	Glu	Asn	Cys	Lys					
				335					340						

<210> 78

<211> 2243

<212> DNA

<213> Homo sapiens

<400> 78

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cgccccctgg cctgcagagg cccgaggacc gcttctgtgg cacatacatc 200

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<210> 79

<211> 475

<212> PRT

<213> Homo sapiens

<400> 79

Met	Ala	Val	Val	Ser	Glu	Asp	Asp	Phe	Gln	His	Ser	Ser	Asn	Ser	1	5	10	15
Thr	Tyr	Gly	Thr	Thr	Ser	Ser	Ser	Leu	Arg	Ala	Asp	Gln	Glu	Ala	20	25	30	
Leu	Leu	Glu	Lys	Leu	Leu	Asp	Arg	Pro	Pro	Pro	Gly	Leu	Gln	Arg	35	40	45	
Pro	Glu	Asp	Arg	Phe	Cys	Gly	Thr	Tyr	Ile	Ile	Phe	Phe	Ser	Leu	50	55	60	
Gly	Ile	Gly	Ser	Leu	Leu	Pro	Trp	Asn	Phe	Phe	Ile	Thr	Ala	Lys	65	70	75	
Glu	Tyr	Trp	Met	Phe	Lys	Leu	Arg	Asn	Ser	Ser	Ser	Pro	Ala	Thr	80	85	90	
Gly	Glu	Asp	Pro	Glu	Gly	Ser	Asp	Ile	Leu	Asn	Tyr	Phe	Glu	Ser	95	100	105	
Tyr	Leu	Ala	Val	Ala	Ser	Thr	Val	Pro	Ser	Met	Leu	Cys	Leu	Val	110	115	120	
Ala	Asn	Phe	Leu	Leu	Val	Asn	Arg	Val	Ala	Val	His	Ile	Arg	Val	125	130	135	

Leu Ala Ser Leu Thr Val Ile Leu Ala Ile Phe Met Val Ile Thr	140	145	150
Ala Leu Val Lys Val Asp Thr Ser Ser Trp Thr Arg Gly Phe Phe	155	160	165
Ala Val Thr Ile Val Cys Met Val Ile Leu Ser Gly Ala Ser Thr	170	175	180
Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser Phe Pro Met	185	190	195
Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly Gly Thr	200	205	210
Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser Asp	215	220	225
Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Ile Phe	230	235	240
Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu	245	250	255
Tyr Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe	260	265	270
Ser Gly Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser	275	280	285
Val Ala Ser Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro	290	295	300
Ile Leu Lys Lys Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val	305	310	315
Phe Phe Ile Thr Ser Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile	320	325	330
Glu Ser Leu Asn Lys Gly Ser Gly Ser Leu Trp Thr Thr Lys Phe	335	340	345
Phe Ile Pro Leu Thr Thr Phe Leu Leu Tyr Asn Phe Ala Asp Leu	350	355	360
Cys Gly Arg Gln Leu Thr Ala Trp Ile Gln Val Pro Gly Pro Asn	365	370	375
Ser Lys Ala Leu Pro Gly Phe Val Leu Leu Arg Thr Cys Leu Ile	380	385	390
Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro Arg Val His Leu Lys	395	400	405
Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala Leu Leu Ser Ser	410	415	420

Leu	Leu	Gly	Leu	Ser	Asn	Gly	Tyr	Leu	Ser	Thr	Leu	Ala	Leu	Leu
				425					430					435
Tyr	Gly	Pro	Lys	Ile	Val	Pro	Arg	Glu	Leu	Ala	Glu	Ala	Thr	Gly
				440					445					450
Val	Val	Met	Ser	Phe	Tyr	Val	Cys	Leu	Gly	Leu	Thr	Leu	Gly	Ser
				455					460					465
Ala	Cys	Ser	Thr	Leu	Leu	Val	His	Leu	Ile					
				470					475					

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 <213> Artificial Sequence

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 <223> Synthetic oligonucleotide probe

<400> 80
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<210> 81
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 81
 cgtaggtgac acagaagccc agg 23

<210> 82
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 82
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<210> 83
 <211> 1844
 <212> DNA
 <213> Homo sapiens

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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1844

<210> 84
<211> 567
<212> PRT
<213> Homo sapiens

<400> 84
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20 25 30
Asp Pro Phe Glu Lys Cys Met Gln Asp Pro Asp Tyr Glu Gln Leu
35 40 45
Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln
50 55 60
Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala
65 70 75
Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala
80 85 90
Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn
95 100 105
Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser
110 115 120
His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu
125 130 135
Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His
140 145 150
Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys
155 160 165
Leu Gly Tyr Ala Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu
170 175 180
Asp Ile Tyr Gln Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys
185 190 195

Ala	Leu	Gly	Cys	Arg	Lys	Ala	Met	Lys	Lys	Phe	Glu	Arg	His	Thr		200	205	210
Leu	Leu	Glu	Tyr	Leu	Leu	Gly	Glu	Gly	Asn	Leu	Ser	Arg	Pro	Ala		215	220	225
Val	Gln	Leu	Leu	Gly	Asp	Val	Met	Ser	Glu	Asp	Gly	Phe	Phe	Tyr		230	235	240
Leu	Ser	Phe	Ala	Glu	Ala	Leu	Arg	Ala	His	Ser	Cys	Leu	Ser	Asp		245	250	255
Arg	Leu	Gln	Tyr	Ser	Arg	Ile	Val	Gly	Gly	Trp	Asp	Leu	Leu	Pro		260	265	270
Arg	Ala	Leu	Leu	Ser	Ser	Leu	Ser	Gly	Leu	Val	Leu	Leu	Asn	Ala		275	280	285
Pro	Val	Val	Ala	Met	Thr	Gln	Gly	Pro	His	Asp	Val	His	Val	Gln		290	295	300
Ile	Glu	Thr	Ser	Pro	Pro	Ala	Arg	Asn	Leu	Lys	Val	Leu	Lys	Ala		305	310	315
Asp	Val	Val	Leu	Leu	Thr	Ala	Ser	Gly	Pro	Ala	Val	Lys	Arg	Ile		320	325	330
Thr	Phe	Ser	Pro	Pro	Leu	Pro	Arg	His	Met	Gln	Glu	Ala	Leu	Arg		335	340	345
Arg	Leu	His	Tyr	Val	Pro	Ala	Thr	Lys	Val	Phe	Leu	Ser	Phe	Arg		350	355	360
Arg	Pro	Phe	Trp	Arg	Glu	Glu	His	Ile	Glu	Gly	Gly	His	Ser	Asn		365	370	375
Thr	Asp	Arg	Pro	Ser	Arg	Met	Ile	Phe	Tyr	Pro	Pro	Pro	Arg	Glu		380	385	390
Gly	Ala	Leu	Leu	Leu	Ala	Ser	Tyr	Thr	Trp	Ser	Asp	Ala	Ala	Ala		395	400	405
Ala	Phe	Ala	Gly	Leu	Ser	Arg	Glu	Glu	Ala	Leu	Arg	Leu	Ala	Leu		410	415	420
Asp	Asp	Val	Ala	Ala	Leu	His	Gly	Pro	Val	Val	Arg	Gln	Leu	Trp		425	430	435
Asp	Gly	Thr	Gly	Val	Val	Lys	Arg	Trp	Ala	Glu	Asp	Gln	His	Ser		440	445	450
Gln	Gly	Gly	Phe	Val	Val	Gln	Pro	Pro	Ala	Leu	Trp	Gln	Thr	Glu		455	460	465
Lys	Asp	Asp	Trp	Thr	Val	Pro	Tyr	Gly	Arg	Ile	Tyr	Phe	Ala	Gly		470	475	480

Glu	His	Thr	Ala	Tyr	Pro	His	Gly	Trp	Val	Glu	Thr	Ala	Val	Lys
				485					490					495
Ser	Ala	Leu	Arg	Ala	Ala	Ile	Lys	Ile	Asn	Ser	Arg	Lys	Gly	Pro
				500					505					510
Ala	Ser	Asp	Thr	Ala	Ser	Pro	Glu	Gly	His	Ala	Ser	Asp	Met	Glu
				515					520					525
Gly	Gln	Gly	His	Val	His	Gly	Val	Ala	Ser	Ser	Pro	Ser	His	Asp
				530					535					540
Leu	Ala	Lys	Glu	Glu	Gly	Ser	His	Pro	Pro	Val	Gln	Gly	Gln	Leu
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Ser	Leu	Gln	Asn	Thr	Thr	His	Thr	Arg	Thr	Ser	His			
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<210> 85
 <211> 3316
 <212> DNA
 <213> Homo sapiens

<400> 85
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<210> 86

<211> 739

<212> PRT

<213> Homo sapiens

<400> 86

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Gly	Lys	Lys	Asp	Arg	Asp	Ser	Cys	Gly	Arg	Lys	Asn	Ser	Glu	Pro
			20						25					30

Gly	Ser	Pro	His	Ser	Leu	Glu	Ala	Leu	Arg	Asp	Ala	Ala	Pro	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35										40					45				
Gln	Gly	Leu	Asn	Phe	Leu	Leu	Leu	Phe	Thr	Lys	Met	Leu	Phe	Ile					
				50					55					60					
Phe	Asn	Phe	Leu	Phe	Ser	Pro	Leu	Pro	Thr	Pro	Ala	Leu	Ile	Cys					
				65					70					75					
Ile	Leu	Thr	Phe	Gly	Ala	Ala	Ile	Phe	Leu	Trp	Leu	Ile	Thr	Arg					
				80					85					90					
Pro	Gln	Pro	Val	Leu	Pro	Leu	Leu	Asp	Leu	Asn	Asn	Gln	Ser	Val					
				95					100					105					
Gly	Ile	Glu	Gly	Gly	Ala	Arg	Lys	Gly	Val	Ser	Gln	Lys	Asn	Asn					
				110					115					120					
Asp	Leu	Thr	Ser	Cys	Cys	Phe	Ser	Asp	Ala	Lys	Thr	Met	Tyr	Glu					
				125					130					135					
Val	Phe	Gln	Arg	Gly	Leu	Ala	Val	Ser	Asp	Asn	Gly	Pro	Cys	Leu					
				140					145					150					
Gly	Tyr	Arg	Lys	Pro	Asn	Gln	Pro	Tyr	Arg	Trp	Leu	Ser	Tyr	Lys					
				155					160					165					
Gln	Val	Ser	Asp	Arg	Ala	Glu	Tyr	Leu	Gly	Ser	Cys	Leu	Leu	His					
				170					175					180					
Lys	Gly	Tyr	Lys	Ser	Ser	Pro	Asp	Gln	Phe	Val	Gly	Ile	Phe	Ala					
				185					190					195					
Gln	Asn	Arg	Pro	Glu	Trp	Ile	Ile	Ser	Glu	Leu	Ala	Cys	Tyr	Thr					
				200					205					210					
Tyr	Ser	Met	Val	Ala	Val	Pro	Leu	Tyr	Asp	Thr	Leu	Gly	Pro	Glu					
				215					220					225					
Ala	Ile	Val	His	Ile	Val	Asn	Lys	Ala	Asp	Ile	Ala	Met	Val	Ile					
				230					235					240					
Cys	Asp	Thr	Pro	Gln	Lys	Ala	Leu	Val	Leu	Ile	Gly	Asn	Val	Glu					
				245					250					255					
Lys	Gly	Phe	Thr	Pro	Ser	Leu	Lys	Val	Ile	Ile	Leu	Met	Asp	Pro					
				260					265					270					
Phe	Asp	Asp	Asp	Leu	Lys	Gln	Arg	Gly	Glu	Lys	Ser	Gly	Ile	Glu					
				275					280					285					
Ile	Leu	Ser	Leu	Tyr	Asp	Ala	Glu	Asn	Leu	Gly	Lys	Glu	His	Phe					
				290					295					300					
Arg	Lys	Pro	Val	Pro	Pro	Ser	Pro	Glu	Asp	Leu	Ser	Val	Ile	Cys					
				305					310					315					
Phe	Thr	Ser	Gly	Thr	Thr	Gly	Asp	Pro	Lys	Gly	Ala	Met	Ile	Thr					

	320		325		330
His Gln Asn Ile Val Ser Asn Ala Ala Ala Phe Leu Lys Cys Val	335		340		345
Glu His Ala Tyr Glu Pro Thr Pro Asp Asp Val Ala Ile Ser Tyr	350		355		360
Leu Pro Leu Ala His Met Phe Glu Arg Ile Val Gln Ala Val Val	365		370		375
Tyr Ser Cys Gly Ala Arg Val Gly Phe Phe Gln Gly Asp Ile Arg	380		385		390
Leu Leu Ala Asp Asp Met Lys Thr Leu Lys Pro Thr Leu Phe Pro	395		400		405
Ala Val Pro Arg Leu Leu Asn Arg Ile Tyr Asp Lys Val Gln Asn	410		415		420
Glu Ala Lys Thr Pro Leu Lys Lys Phe Leu Leu Lys Leu Ala Val	425		430		435
Ser Ser Lys Phe Lys Glu Leu Gln Lys Gly Ile Ile Arg His Asp	440		445		450
Ser Phe Trp Asp Lys Leu Ile Phe Ala Lys Ile Gln Asp Ser Leu	455		460		465
Gly Gly Arg Val Arg Val Ile Val Thr Gly Ala Ala Pro Met Ser	470		475		480
Thr Ser Val Met Thr Phe Phe Arg Ala Ala Met Gly Cys Gln Val	485		490		495
Tyr Glu Ala Tyr Gly Gln Thr Glu Cys Thr Gly Gly Cys Thr Phe	500		505		510
Thr Leu Pro Gly Asp Trp Thr Ser Gly His Val Gly Val Pro Leu	515		520		525
Ala Cys Asn Tyr Val Lys Leu Glu Asp Val Ala Asp Met Asn Tyr	530		535		540
Phe Thr Val Asn Asn Glu Gly Glu Val Cys Ile Lys Gly Thr Asn	545		550		555
Val Phe Lys Gly Tyr Leu Lys Asp Pro Glu Lys Thr Gln Glu Ala	560		565		570
Leu Asp Ser Asp Gly Trp Leu His Thr Gly Asp Ile Gly Arg Trp	575		580		585
Leu Pro Asn Gly Thr Leu Lys Ile Ile Asp Arg Lys Lys Asn Ile	590		595		600
Phe Lys Leu Ala Gln Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu					

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Asn	Ile	Tyr	Asn	Arg	Ser	Gln	Pro	Val	Leu	Gln	Ile	Phe	Val	His
			620						625					630
Gly	Glu	Ser	Leu	Arg	Ser	Ser	Leu	Val	Gly	Val	Val	Val	Pro	Asp
			635						640					645
Thr	Asp	Val	Leu	Pro	Ser	Phe	Ala	Ala	Lys	Leu	Gly	Val	Lys	Gly
			650						655					660
Ser	Phe	Glu	Glu	Leu	Cys	Gln	Asn	Gln	Val	Val	Arg	Glu	Ala	Ile
			665						670					675
Leu	Glu	Asp	Leu	Gln	Lys	Ile	Gly	Lys	Glu	Ser	Gly	Leu	Lys	Thr
			680						685					690
Phe	Glu	Gln	Val	Lys	Ala	Ile	Phe	Leu	His	Pro	Glu	Pro	Phe	Ser
			695						700					705
Ile	Glu	Asn	Gly	Leu	Leu	Thr	Pro	Thr	Leu	Lys	Ala	Lys	Arg	Gly
			710						715					720
Glu	Leu	Ser	Lys	Tyr	Phe	Arg	Thr	Gln	Ile	Asp	Ser	Leu	Tyr	Glu
			725						730					735

His Ile Gln Asp

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 <211> 2725
 <212> DNA
 <213> Homo sapiens

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 cccctcatca agccctttgg ggctcggaag aagcggagct ggtaccttac 200
 ctggaagtat aaactgacaa accagcgggc cctgcggaga ttctgtcaga 250
 caggggccgt gcttttctg ctggtgactg tcattgtcaa tatcaagttg 300
 atcctggaca ctgcgcgagc catcagtga gccaatgaag acccagagcc 350
 agagcaagac tatgatgagg ccctaggccg cctggagccc ccacggcgca 400
 gaggcagtgg tccccggcgg gtccctggacg tagaggtgta ttcaagtcgc 450
 agcaaagtat atgtggcagt ggatggcacc acggtgctgg aggatgaggg 500
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 aaaaaaaaaa aaaaaaaaaa aaaaa 2725

<210> 88
 <211> 660
 <212> PRT
 <213> Homo sapiens

<400> 88
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 Asn Gln Arg Ala Leu Arg Arg Phe Cys Gln Thr Gly Ala Val Leu
 35 40 45
 Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp
 50 55 60
 Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu
 65 70 75
 Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg
 80 85 90
 Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser
 95 100 105

Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu	110	115	120
Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val	125	130	135
Leu Asn Gln Ala Thr Gly His Val Met Ala Lys Arg Val Phe Asp	140	145	150
Thr Tyr Ser Pro His Glu Asp Glu Ala Met Val Leu Phe Leu Asn	155	160	165
Met Val Ala Pro Gly Arg Val Leu Ile Cys Thr Val Lys Asp Glu	170	175	180
Gly Ser Phe His Leu Lys Asp Thr Ala Lys Ala Leu Leu Arg Ser	185	190	195
Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly Trp Arg Asp Thr Trp	200	205	210
Ala Phe Val Gly Arg Lys Gly Gly Pro Val Phe Gly Glu Lys His	215	220	225
Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly Asp Pro Val Leu Leu	230	235	240
Lys Thr Asp Val Pro Leu Ser Ser Ala Glu Glu Ala Glu Cys His	245	250	255
Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg Arg Arg Phe Cys Ser	260	265	270
Lys Val Glu Gly Tyr Gly Ser Val Cys Ser Cys Lys Asp Pro Thr	275	280	285
Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro Asp Asn Lys Val Leu	290	295	300
Asn Val Pro Val Ala Val Ile Ala Gly Asn Arg Pro Asn Tyr Leu	305	310	315
Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala Gln Gly Val Ser Pro	320	325	330
Gln Met Ile Thr Val Phe Ile Asp Gly Tyr Tyr Glu Glu Pro Met	335	340	345
Asp Val Val Ala Leu Phe Gly Leu Arg Gly Ile Gln His Thr Pro	350	355	360
Ile Ser Ile Lys Asn Ala Arg Val Ser Gln His Tyr Lys Ala Ser	365	370	375
Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu Ala Lys Phe Ala Val	380	385	390

Val	Leu	Glu	Glu	Asp	Leu	Asp	Ile	Ala	Val	Asp	Phe	Phe	Ser	Phe			395	400	405
Leu	Ser	Gln	Ser	Ile	His	Leu	Leu	Glu	Glu	Asp	Asp	Ser	Leu	Tyr			410	415	420
Cys	Ile	Ser	Ala	Trp	Asn	Asp	Gln	Gly	Tyr	Glu	His	Thr	Ala	Glu			425	430	435
Asp	Pro	Ala	Leu	Leu	Tyr	Arg	Val	Glu	Thr	Met	Pro	Gly	Leu	Gly			440	445	450
Trp	Val	Leu	Arg	Arg	Ser	Leu	Tyr	Lys	Glu	Glu	Leu	Glu	Pro	Lys			455	460	465
Trp	Pro	Thr	Pro	Glu	Lys	Leu	Trp	Asp	Trp	Asp	Met	Trp	Met	Arg			470	475	480
Met	Pro	Glu	Gln	Arg	Arg	Gly	Arg	Glu	Cys	Ile	Ile	Pro	Asp	Val			485	490	495
Ser	Arg	Ser	Tyr	His	Phe	Gly	Ile	Val	Gly	Leu	Asn	Met	Asn	Gly			500	505	510
Tyr	Phe	His	Glu	Ala	Tyr	Phe	Lys	Lys	His	Lys	Phe	Asn	Thr	Val			515	520	525
Pro	Gly	Val	Gln	Leu	Arg	Asn	Val	Asp	Ser	Leu	Lys	Lys	Glu	Ala			530	535	540
Tyr	Glu	Val	Glu	Val	His	Arg	Leu	Leu	Ser	Glu	Ala	Glu	Val	Leu			545	550	555
Asp	His	Ser	Lys	Asn	Pro	Cys	Glu	Asp	Ser	Phe	Leu	Pro	Asp	Thr			560	565	570
Glu	Gly	His	Thr	Tyr	Val	Ala	Phe	Ile	Arg	Met	Glu	Lys	Asp	Asp			575	580	585
Asp	Phe	Thr	Thr	Trp	Thr	Gln	Leu	Ala	Lys	Cys	Leu	His	Ile	Trp			590	595	600
Asp	Leu	Asp	Val	Arg	Gly	Asn	His	Arg	Gly	Leu	Trp	Arg	Leu	Phe			605	610	615
Arg	Lys	Lys	Asn	His	Phe	Leu	Val	Val	Gly	Val	Pro	Ala	Ser	Pro			620	625	630
Tyr	Ser	Val	Lys	Lys	Pro	Pro	Ser	Val	Thr	Pro	Ile	Phe	Leu	Glu			635	640	645
Pro	Pro	Pro	Lys	Glu	Glu	Gly	Ala	Pro	Gly	Ala	Pro	Glu	Gln	Thr			650	655	660

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<211> 25

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 89
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<210> 90
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 90
cctcaaccag gccacgggcc ac 22

<210> 91
<211> 24
<212> DNA
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 91
cccaggcaga gatgcagtac aggc 24

<210> 92
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<400> 92
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<210> 93
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<212> DNA
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<210> 94
<211> 3037
<212> DNA
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<400> 94

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<211> 307

<212> PRT

<213> Homo sapiens

<400> 95

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Ser	Glu	Glu	Arg	Leu	Lys	Leu	Val	Thr	Val	Leu	Gly	Ala	Gly	Leu	35	40	45	
Leu	Cys	Gly	Thr	Ala	Leu	Ala	Val	Ile	Val	Pro	Glu	Gly	Val	His	50	55	60	
Ala	Leu	Tyr	Glu	Asp	Ile	Leu	Glu	Gly	Lys	His	His	Gln	Ala	Ser	65	70	75	
Glu	Thr	His	Asn	Val	Ile	Ala	Ser	Asp	Lys	Ala	Ala	Glu	Lys	Ser	80	85	90	
Val	Val	His	Glu	His	Glu	His	Ser	His	Asp	His	Thr	Gln	Leu	His	95	100	105	
Ala	Tyr	Ile	Gly	Val	Ser	Leu	Val	Leu	Gly	Phe	Val	Phe	Met	Leu	110	115	120	
Leu	Val	Asp	Gln	Ile	Gly	Asn	Ser	His	Val	His	Ser	Thr	Asp	Asp	125	130	135	
Pro	Glu	Ala	Ala	Arg	Ser	Ser	Asn	Ser	Lys	Ile	Thr	Thr	Thr	Leu	140	145	150	
Gly	Leu	Val	Val	His	Ala	Ala	Ala	Asp	Gly	Val	Ala	Leu	Gly	Ala	155	160	165	
Ala	Ala	Ser	Thr	Ser	Gln	Thr	Ser	Val	Gln	Leu	Ile	Val	Phe	Val	170	175	180	
Ala	Ile	Met	Leu	His	Lys	Ala	Pro	Ala	Ala	Phe	Gly	Leu	Val	Ser	185	190	195	
Phe	Leu	Met	His	Ala	Gly	Leu	Glu	Arg	Asn	Arg	Ile	Arg	Lys	His	200	205	210	

Leu	Leu	Val	Phe	Ala	Leu	Ala	Ala	Pro	Val	Met	Ser	Met	Val	Thr
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Tyr	Leu	Gly	Leu	Ser	Lys	Ser	Ser	Lys	Glu	Ala	Leu	Ser	Glu	Val
				230					235					240
Asn	Ala	Thr	Gly	Val	Ala	Met	Leu	Phe	Ser	Ala	Gly	Thr	Phe	Leu
				245					250					255
Tyr	Val	Ala	Thr	Val	His	Val	Leu	Pro	Glu	Val	Gly	Gly	Ile	Gly
				260					265					270
His	Ser	His	Lys	Pro	Asp	Ala	Thr	Gly	Gly	Arg	Gly	Leu	Ser	Arg
				275					280					285
Leu	Glu	Val	Ala	Ala	Leu	Val	Leu	Gly	Cys	Leu	Ile	Pro	Leu	Ile
				290					295					300
Leu	Ser	Val	Gly	His	Gln	His								
				305										

<210> 96
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 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

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<210> 97
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 97
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<210> 98
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
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<210> 99
 <211> 1429

<212> DNA

<213> Homo sapiens

<400> 99

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ctgattttga gatgatgggc ttgggaaacg ggcgtcgcag catgaagtcg 150
ccgccccctcg tgctggccgc cctggtggcc tgcatcatcg tcttgggctt 200
caactactgg attgcgagct cccggagcgt ggacctccag acacggatca 250
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gagctgaaga agaacgagtt ccagggagag ctggagaagc agcgggagca 350
gcttgacaaa atccagtcca gccacaactt ccagctggag agcgtcaaca 400
agctgtacca ggacgaaaag gcggttttgg tgaataacat caccacaggt 450
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ggaatcatat actctgaatt gaactggaat cacatatttc acaacagggc 1350

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<210> 100

<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

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Leu	Val	Leu	Ala	Ala	Leu	Val	Ala	Cys	Ile	Ile	Val	Leu	Gly	Phe
			20						25					30

Asn	Tyr	Trp	Ile	Ala	Ser	Ser	Arg	Ser	Val	Asp	Leu	Gln	Thr	Arg
			35						40					45

Ile	Met	Glu	Leu	Glu	Gly	Arg	Val	Arg	Arg	Ala	Ala	Ala	Glu	Arg
			50						55					60

Gly	Ala	Val	Glu	Leu	Lys	Lys	Asn	Glu	Phe	Gln	Gly	Glu	Leu	Glu
			65						70					75

Lys	Gln	Arg	Glu	Gln	Leu	Asp	Lys	Ile	Gln	Ser	Ser	His	Asn	Phe
			80						85					90

Gln	Leu	Glu	Ser	Val	Asn	Lys	Leu	Tyr	Gln	Asp	Glu	Lys	Ala	Val
			95						100					105

Leu	Val	Asn	Asn	Ile	Thr	Thr	Gly	Glu	Arg	Leu	Ile	Arg	Val	Leu
			110						115					120

Gln	Asp	Gln	Leu	Lys	Thr	Leu	Gln	Arg	Asn	Tyr	Gly	Arg	Leu	Gln
			125						130					135

Gln	Asp	Val	Leu	Gln	Phe	Gln	Lys	Asn	Gln	Thr	Asn	Leu	Glu	Arg
			140						145					150

Lys	Phe	Ser	Tyr	Asp	Leu	Ser	Gln	Cys	Ile	Asn	Gln	Met	Lys	Glu
			155						160					165

Val	Lys	Glu	Gln	Cys	Glu	Glu	Arg	Ile	Glu	Glu	Val	Thr	Lys	Lys
			170						175					180

Gly	Asn	Glu	Ala	Val	Ala	Ser	Arg	Asp	Leu	Ser	Glu	Asn	Asn	Asp
			185						190					195

Gln	Arg	Gln	Gln	Leu	Gln	Ala	Leu	Ser	Glu	Pro	Gln	Pro	Arg	Leu
			200						205					210

Gln	Ala	Ala	Gly	Leu	Pro	His	Thr	Glu	Val	Pro	Gln	Gly	Lys	Gly
			215						220					225

Asn Val Leu Gly Asn Ser Lys Ser Gln Thr Pro Ala Pro Ser Ser

230	235	240
Glu Val Val Leu Asp Ser Lys Arg Gln Val Glu Lys Glu Glu Thr		
245	250	255
Asn Glu Ile Gln Val Val Asn Glu Glu Pro Gln Arg Asp Arg Leu		
260	265	270
Pro Gln Glu Pro Gly Arg Glu Gln Val Val Glu Asp Arg Pro Val		
275	280	285
Gly Gly Arg Gly Phe Gly Gly Ala Gly Glu Leu Gly Gln Thr Pro		
290	295	300
Gln Val Gln Ala Ala Leu Ser Val Ser Gln Glu Asn Pro Glu Met		
305	310	315
Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro Asp Gly Gln Glu		
320	325	330
Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn Gln Gln Lys Leu		
335	340	345
Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala Glu Ser		
350	355	360
Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn Ile		
365	370	375
Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr Ile Asn Leu		
380	385	390
Leu Asp Gln Arg Glu Lys Arg Asn His Thr Leu		
395	400	

<210> 101
 <211> 3671
 <212> DNA
 <213> Homo sapiens

<400> 101
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<210> 102

<211> 1089

<212> PRT

<213> Homo sapiens

<400> 102

Met	Gln	Lys	Ala	Ser	Val	Leu	Leu	Phe	Leu	Ala	Trp	Val	Cys	Phe	1	5	10	15
Leu	Phe	Tyr	Ala	Gly	Ile	Ala	Leu	Phe	Thr	Ser	Gly	Phe	Leu	Leu	20	25	30	
Thr	Arg	Leu	Glu	Leu	Thr	Asn	His	Ser	Ser	Cys	Gln	Glu	Pro	Pro	35	40	45	
Gly	Pro	Gly	Ser	Leu	Pro	Trp	Gly	Ser	Gln	Gly	Lys	Pro	Gly	Ala	50	55	60	
Cys	Trp	Met	Ala	Ser	Arg	Phe	Ser	Arg	Val	Val	Leu	Val	Leu	Ile	65	70	75	
Asp	Ala	Leu	Arg	Phe	Asp	Phe	Ala	Gln	Pro	Gln	His	Ser	His	Val	80	85	90	
Pro	Arg	Glu	Pro	Pro	Val	Ser	Leu	Pro	Phe	Leu	Gly	Lys	Leu	Ser	95	100	105	
Ser	Leu	Gln	Arg	Ile	Leu	Glu	Ile	Gln	Pro	His	His	Ala	Arg	Leu	110	115	120	
Tyr	Arg	Ser	Gln	Val	Asp	Pro	Pro	Thr	Thr	Thr	Met	Gln	Arg	Leu	125	130	135	
Lys	Ala	Leu	Thr	Thr	Gly	Ser	Leu	Pro	Thr	Phe	Ile	Asp	Ala	Gly	140	145	150	
Ser	Asn	Phe	Ala	Ser	His	Ala	Ile	Val	Glu	Asp	Asn	Leu	Ile	Lys	155	160	165	

Gln	Leu	Thr	Ser	Ala	Gly	Arg	Arg	Val	Val	Phe	Met	Gly	Asp	Asp	
				170					175					180	
Thr	Trp	Lys	Asp	Leu	Phe	Pro	Gly	Ala	Phe	Ser	Lys	Ala	Phe	Phe	
				185					190					195	
Phe	Pro	Ser	Phe	Asn	Val	Arg	Asp	Leu	Asp	Thr	Val	Asp	Asn	Gly	
				200					205					210	
Ile	Leu	Glu	His	Leu	Tyr	Pro	Thr	Met	Asp	Ser	Gly	Glu	Trp	Asp	
				215					220					225	
Val	Leu	Ile	Ala	His	Phe	Leu	Gly	Val	Asp	His	Cys	Gly	His	Lys	
				230					235					240	
His	Gly	Pro	His	His	Pro	Glu	Met	Ala	Lys	Lys	Leu	Ser	Gln	Met	
				245					250					255	
Asp	Gln	Val	Ile	Gln	Gly	Leu	Val	Glu	Arg	Leu	Glu	Asn	Asp	Thr	
				260					265					270	
Leu	Leu	Val	Val	Ala	Gly	Asp	His	Gly	Met	Thr	Thr	Asn	Gly	Asp	
				275					280					285	
His	Gly	Gly	Asp	Ser	Glu	Leu	Glu	Val	Ser	Ala	Ala	Leu	Phe	Leu	
				290					295					300	
Tyr	Ser	Pro	Thr	Ala	Val	Phe	Pro	Ser	Thr	Pro	Pro	Glu	Glu	Pro	
				305					310					315	
Glu	Val	Ile	Pro	Gln	Val	Ser	Leu	Val	Pro	Thr	Leu	Ala	Leu	Leu	
				320					325					330	
Leu	Gly	Leu	Pro	Ile	Pro	Phe	Gly	Asn	Ile	Gly	Glu	Val	Met	Ala	
				335					340					345	
Glu	Leu	Phe	Ser	Gly	Gly	Glu	Asp	Ser	Gln	Pro	His	Ser	Ser	Ala	
				350					355					360	
Leu	Ala	Gln	Ala	Ser	Ala	Leu	His	Leu	Asn	Ala	Gln	Gln	Val	Ser	
				365					370					375	
Arg	Phe	Leu	His	Thr	Tyr	Ser	Ala	Ala	Thr	Gln	Asp	Leu	Gln	Ala	
				380					385					390	
Lys	Glu	Leu	His	Gln	Leu	Gln	Asn	Leu	Phe	Ser	Lys	Ala	Ser	Ala	
				395					400					405	
Asp	Tyr	Gln	Trp	Leu	Leu	Gln	Ser	Pro	Lys	Gly	Ala	Glu	Ala	Thr	
				410					415					420	
Leu	Pro	Thr	Val	Ile	Ala	Glu	Leu	Gln	Gln	Phe	Leu	Arg	Gly	Ala	
				425					430					435	
Arg	Ala	Met	Cys	Ile	Glu	Ser	Trp	Ala	Arg	Phe	Ser	Leu	Val	Arg	
				440					445					450	

Met	Ala	Gly	Gly	Thr	Ala	Leu	Leu	Ala	Ala	Ser	Cys	Phe	Ile	Cys	455	460	465
Leu	Leu	Ala	Ser	Gln	Trp	Ala	Ile	Ser	Pro	Gly	Phe	Pro	Phe	Cys	470	475	480
Pro	Leu	Leu	Leu	Thr	Pro	Val	Ala	Trp	Gly	Leu	Val	Gly	Ala	Ile	485	490	495
Ala	Tyr	Ala	Gly	Leu	Leu	Gly	Thr	Ile	Glu	Leu	Lys	Leu	Asp	Leu	500	505	510
Val	Leu	Leu	Gly	Ala	Val	Ala	Ala	Val	Ser	Ser	Phe	Leu	Pro	Phe	515	520	525
Leu	Trp	Lys	Ala	Trp	Ala	Gly	Trp	Gly	Ser	Lys	Arg	Pro	Leu	Ala	530	535	540
Thr	Leu	Phe	Pro	Ile	Pro	Gly	Pro	Val	Leu	Leu	Leu	Leu	Leu	Phe	545	550	555
Arg	Leu	Ala	Val	Phe	Phe	Ser	Asp	Ser	Phe	Val	Val	Ala	Glu	Ala	560	565	570
Arg	Ala	Thr	Pro	Phe	Leu	Leu	Gly	Ser	Phe	Ile	Leu	Leu	Leu	Val	575	580	585
Val	Gln	Leu	His	Trp	Glu	Gly	Gln	Leu	Leu	Pro	Pro	Lys	Leu	Leu	590	595	600
Thr	Met	Pro	Arg	Leu	Gly	Thr	Ser	Ala	Thr	Thr	Asn	Pro	Pro	Arg	605	610	615
His	Asn	Gly	Ala	Tyr	Ala	Leu	Arg	Leu	Gly	Ile	Gly	Leu	Leu	Leu	620	625	630
Cys	Thr	Arg	Leu	Ala	Gly	Leu	Phe	His	Arg	Cys	Pro	Glu	Glu	Thr	635	640	645
Pro	Val	Cys	His	Ser	Ser	Pro	Trp	Leu	Ser	Pro	Leu	Ala	Ser	Met	650	655	660
Val	Gly	Gly	Arg	Ala	Lys	Asn	Leu	Trp	Tyr	Gly	Ala	Cys	Val	Ala	665	670	675
Ala	Leu	Val	Ala	Leu	Leu	Ala	Ala	Val	Arg	Leu	Trp	Leu	Arg	Arg	680	685	690
Tyr	Gly	Asn	Leu	Lys	Ser	Pro	Glu	Pro	Pro	Met	Leu	Phe	Val	Arg	695	700	705
Trp	Gly	Leu	Pro	Leu	Met	Ala	Leu	Gly	Thr	Ala	Ala	Tyr	Trp	Ala	710	715	720
Leu	Ala	Ser	Gly	Ala	Asp	Glu	Ala	Pro	Pro	Arg	Leu	Arg	Val	Leu	725	730	735

Val Ser Gly Ala	Ser Met Val Leu Pro	Arg Ala Val Ala Gly	Leu
740		745	750
Ala Ala Ser Gly	Leu Ala Leu Leu Leu	Trp Lys Pro Val Thr	Val
755		760	765
Leu Val Lys Ala	Gly Ala Gly Ala Pro	Arg Thr Arg Thr Val	Leu
770		775	780
Thr Pro Phe Ser	Gly Pro Pro Thr Ser	Gln Ala Asp Leu Asp	Tyr
785		790	795
Val Val Pro Gln	Ile Tyr Arg His Met	Gln Glu Glu Phe Arg	Gly
800		805	810
Arg Leu Glu Arg	Thr Lys Ser Gln Gly	Pro Leu Thr Val Ala	Ala
815		820	825
Tyr Gln Leu Gly	Ser Val Tyr Ser Ala	Ala Met Val Thr Ala	Leu
830		835	840
Thr Leu Leu Ala	Phe Pro Leu Leu Leu	Leu His Ala Glu Arg	Ile
845		850	855
Ser Leu Val Phe	Leu Leu Leu Phe Leu	Gln Ser Phe Leu Leu	Leu
860		865	870
His Leu Leu Ala	Ala Gly Ile Pro Val	Thr Thr Pro Gly Pro	Phe
875		880	885
Thr Val Pro Trp	Gln Ala Val Ser Ala	Trp Ala Leu Met Ala	Thr
890		895	900
Gln Thr Phe Tyr	Ser Thr Gly His Gln	Pro Val Phe Pro Ala	Ile
905		910	915
His Trp His Ala	Ala Phe Val Gly Phe	Pro Glu Gly His Gly	Ser
920		925	930
Cys Thr Trp Leu	Pro Ala Leu Leu Val	Gly Ala Asn Thr Phe	Ala
935		940	945
Ser His Leu Leu	Phe Ala Val Gly Cys	Pro Leu Leu Leu Leu	Trp
950		955	960
Pro Phe Leu Cys	Glu Ser Gln Gly Leu	Arg Lys Arg Gln Gln	Pro
965		970	975
Pro Gly Asn Glu	Ala Asp Ala Arg Val	Arg Pro Glu Glu Glu	Glu
980		985	990
Glu Pro Leu Met	Glu Met Arg Leu Arg	Asp Ala Pro Gln His	Phe
995		1000	1005
Tyr Ala Ala Leu	Leu Gln Leu Gly Leu	Lys Tyr Leu Phe Ile	Leu
1010		1015	1020

Gly Ile Gln Ile Leu Ala Cys Ala Leu Ala Ala Ser Ile Leu Arg		
1025	1030	1035
Arg His Leu Met Val Trp Lys Val Phe Ala Pro Lys Phe Ile Phe		
1040	1045	1050
Glu Ala Val Gly Phe Ile Val Ser Ser Val Gly Leu Leu Leu Gly		
1055	1060	1065
Ile Ala Leu Val Met Arg Val Asp Gly Ala Val Ser Ser Trp Phe		
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Arg Gln Leu Phe Leu Ala Gln Gln Arg		
1085		

<210> 103
 <211> 1743
 <212> DNA
 <213> Homo sapiens

<400> 103
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 ttcaaggagt taaagttact tacactgtgc agtatttcat cacaaattgg 200
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 atttctcatc aggatatgag tttactggga aaaagcagtg atgtatccag 800
 ccttaatgat cctcagccca gcgggaacct gaggccccct caggaggaag 850
 aggaggtgaa acatttaggg tatgcttcgc atttgatgga aattttttgt 900

gactctgaag aaaacacgga aggtacttct ctcacccagc aagagtcctt 950
cagcagaaca atacccccgg ataaaacagt cattgaatat gaatatgatg 1000
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cgtgtgtgat tgggtcatgc atgtaggtct cttacaatg atgggtgggc 1650
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<210> 104

<211> 442

<212> PRT

<213> Homo sapiens

<400> 104

Met	Ser	Tyr	Asn	Gly	Leu	His	Gln	Arg	Val	Phe	Lys	Glu	Leu	Lys
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Leu	Leu	Thr	Leu	Cys	Ser	Ile	Ser	Ser	Gln	Ile	Gly	Pro	Pro	Glu
				20					25					30
Val	Ala	Leu	Thr	Thr	Asp	Glu	Lys	Ser	Ile	Ser	Val	Val	Leu	Thr
				35					40					45
Ala	Pro	Glu	Lys	Trp	Lys	Arg	Asn	Pro	Glu	Asp	Leu	Pro	Val	Ser
				50					55					60
Met	Gln	Gln	Ile	Tyr	Ser	Asn	Leu	Lys	Tyr	Asn	Val	Ser	Val	Leu
				65					70					75
Asn	Thr	Lys	Ser	Asn	Arg	Thr	Trp	Ser	Gln	Cys	Val	Thr	Asn	His
				80					85					90

Thr	Leu	Val	Leu	Thr	Trp	Leu	Glu	Pro	Asn	Thr	Leu	Tyr	Cys	Val	95	100	105
His	Val	Glu	Ser	Phe	Val	Pro	Gly	Pro	Pro	Arg	Arg	Ala	Gln	Pro	110	115	120
Ser	Glu	Lys	Gln	Cys	Ala	Arg	Thr	Leu	Lys	Asp	Gln	Ser	Ser	Glu	125	130	135
Phe	Lys	Ala	Lys	Ile	Ile	Phe	Trp	Tyr	Val	Leu	Pro	Ile	Ser	Ile	140	145	150
Thr	Val	Phe	Leu	Phe	Ser	Val	Met	Gly	Tyr	Ser	Ile	Tyr	Arg	Tyr	155	160	165
Ile	His	Val	Gly	Lys	Glu	Lys	His	Pro	Ala	Asn	Leu	Ile	Leu	Ile	170	175	180
Tyr	Gly	Asn	Glu	Phe	Asp	Lys	Arg	Phe	Phe	Val	Pro	Ala	Glu	Lys	185	190	195
Ile	Val	Ile	Asn	Phe	Ile	Thr	Leu	Asn	Ile	Ser	Asp	Asp	Ser	Lys	200	205	210
Ile	Ser	His	Gln	Asp	Met	Ser	Leu	Leu	Gly	Lys	Ser	Ser	Asp	Val	215	220	225
Ser	Ser	Leu	Asn	Asp	Pro	Gln	Pro	Ser	Gly	Asn	Leu	Arg	Pro	Pro	230	235	240
Gln	Glu	Glu	Glu	Glu	Val	Lys	His	Leu	Gly	Tyr	Ala	Ser	His	Leu	245	250	255
Met	Glu	Ile	Phe	Cys	Asp	Ser	Glu	Glu	Asn	Thr	Glu	Gly	Thr	Ser	260	265	270
Leu	Thr	Gln	Gln	Glu	Ser	Leu	Ser	Arg	Thr	Ile	Pro	Pro	Asp	Lys	275	280	285
Thr	Val	Ile	Glu	Tyr	Glu	Tyr	Asp	Val	Arg	Thr	Thr	Asp	Ile	Cys	290	295	300
Ala	Gly	Pro	Glu	Glu	Gln	Glu	Leu	Ser	Leu	Gln	Glu	Glu	Val	Ser	305	310	315
Thr	Gln	Gly	Thr	Leu	Leu	Glu	Ser	Gln	Ala	Ala	Leu	Ala	Val	Leu	320	325	330
Gly	Pro	Gln	Thr	Leu	Gln	Tyr	Ser	Tyr	Thr	Pro	Gln	Leu	Gln	Asp	335	340	345
Leu	Asp	Pro	Leu	Ala	Gln	Glu	His	Thr	Asp	Ser	Glu	Glu	Gly	Pro	350	355	360
Glu	Glu	Glu	Pro	Ser	Thr	Thr	Leu	Val	Asp	Trp	Asp	Pro	Gln	Thr	365	370	375

Gly Arg Leu Cys Ile Pro Ser Leu Ser Ser Phe Asp Gln Asp Ser
380 385 390

Glu Gly Cys Glu Pro Ser Glu Gly Asp Gly Leu Gly Glu Glu Gly
395 400 405

Leu Leu Ser Arg Leu Tyr Glu Glu Pro Ala Pro Asp Arg Pro Pro
410 415 420

Gly Glu Asn Glu Thr Tyr Leu Met Gln Phe Met Glu Glu Trp Gly
425 430 435

Leu Tyr Val Gln Met Glu Asn
440

<210> 105

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 105

cgctgctgct gttgctcctg g 21

<210> 106

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 106

cagtgtgccca ggactttg 18

<210> 107

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 107

agtcgcaggc agcgttgg 18

<210> 108

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 108
ctcctccgag tctgtgtgct cctgc 25

<210> 109

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 109

ggacgggcag ttccctgtgt ctctggtggt ttgcctaaac ctgcaaacat 50

c 51

<210> 110

<211> 1114

<212> DNA

<213> Homo sapiens

<400> 110

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cgccagcctg cgtctgccat ggggctcggg ttgaggggct ggggacgtcc 100
tctgtctgact gtggccaccg ccctgatgct gcccgtaag cccccgcag 150
gctcctgggg ggcccagatc atcgggggcc acgaggtgac cccccactcc 200
aggccctaca tggcatccgt gcgcttcggg ggccaacatc actgcggagg 250
cttcctgctg cgagcccgt ggggtgtctc ggccgcccac tgcttcagcc 300
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 tggttcagggg tgggggtggga cgggcagcgg tggggcacac ccattccaca 1050
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 aaaaaaaaaa gaaa 1114

<210> 111
 <211> 283
 <212> PRT
 <213> Homo sapiens

<400> 111
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 Ala Thr Ala Leu Met Leu Pro Val Lys Pro Pro Ala Gly Ser Trp
 20 25 30
 Gly Ala Gln Ile Ile Gly Gly His Glu Val Thr Pro His Ser Arg
 35 40 45
 Pro Tyr Met Ala Ser Val Arg Phe Gly Gly Gln His His Cys Gly
 50 55 60
 Gly Phe Leu Leu Arg Ala Arg Trp Val Val Ser Ala Ala His Cys
 65 70 75
 Phe Ser His Arg Asp Leu Arg Thr Gly Leu Val Val Leu Gly Ala
 80 85 90
 His Val Leu Ser Thr Ala Glu Pro Thr Gln Gln Val Phe Gly Ile
 95 100 105
 Asp Ala Leu Thr Thr His Pro Asp Tyr His Pro Met Thr His Ala
 110 115 120
 Asn Asp Ile Cys Leu Leu Arg Leu Asn Gly Ser Ala Val Leu Gly
 125 130 135
 Pro Ala Val Gly Leu Leu Arg Leu Pro Gly Arg Arg Ala Arg Pro
 140 145 150
 Pro Thr Ala Gly Thr Arg Cys Arg Val Ala Gly Trp Gly Phe Val
 155 160 165
 Ser Asp Phe Glu Glu Leu Pro Pro Gly Leu Met Glu Ala Lys Val
 170 175 180
 Arg Val Leu Asp Pro Asp Val Cys Asn Ser Ser Trp Lys Gly His
 185 190 195
 Leu Thr Leu Thr Met Leu Cys Thr Arg Ser Gly Asp Ser His Arg

	200	205	210
Arg Gly Phe Cys	Ser Ala Asp Ser Gly	Gly Pro Leu Val Cys	Arg
	215	220	225
Asn Arg Ala His	Gly Leu Val Ser Phe	Ser Gly Leu Trp Cys	Gly
	230	235	240
Asp Pro Lys Thr	Pro Asp Val Tyr Thr	Gln Val Ser Ala Phe	Val
	245	250	255
Ala Trp Ile Trp	Asp Val Val Arg Arg	Ser Ser Pro Gln Pro	Gly
	260	265	270
Pro Leu Pro Gly	Thr Thr Arg Pro Pro	Gly Glu Ala Ala	
	275	280	

<210> 112

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 112

gacgtctgca acagctcctg gaag 24

<210> 113

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 113

cgagaaggaa acgaggccgt gag 23

<210> 114

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 114

tgacacttac catgctctgc acccgcagtg gggacagcca caga 44

<210> 115

<211> 1808

<212> DNA

<213> Homo sapiens

<400> 115

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cgctgtcggc gctgggcacg gtagcaggcg ccgccgtgct gctcaaggac 150
tatgtcaccg gtggggcttg cccagcaag gccaccatcc ctgggaagac 200
ggtcatcgtg acgggcgcca acacaggcat cgggaagcag accgccttgg 250
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aagtgtgagg cggcagcaaa ggacatccgc ggggagaccc tcaatcacca 350
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gctcattt 1808

<210> 116

<211> 331

<212> PRT

<213> Homo sapiens

<400> 116

Met	Ser	Arg	Tyr	Leu	Leu	Pro	Leu	Ser	Ala	Leu	Gly	Thr	Val	Ala	1	5	10	15
Gly	Ala	Ala	Val	Leu	Leu	Lys	Asp	Tyr	Val	Thr	Gly	Gly	Ala	Cys	20	25	30	
Pro	Ser	Lys	Ala	Thr	Ile	Pro	Gly	Lys	Thr	Val	Ile	Val	Thr	Gly	35	40	45	
Ala	Asn	Thr	Gly	Ile	Gly	Lys	Gln	Thr	Ala	Leu	Glu	Leu	Ala	Arg	50	55	60	
Arg	Gly	Gly	Asn	Ile	Ile	Leu	Ala	Cys	Arg	Asp	Met	Glu	Lys	Cys	65	70	75	
Glu	Ala	Ala	Ala	Lys	Asp	Ile	Arg	Gly	Glu	Thr	Leu	Asn	His	His	80	85	90	
Val	Asn	Ala	Arg	His	Leu	Asp	Leu	Ala	Ser	Leu	Lys	Ser	Ile	Arg	95	100	105	
Glu	Phe	Ala	Ala	Lys	Ile	Ile	Glu	Glu	Glu	Glu	Arg	Val	Asp	Ile	110	115	120	
Leu	Ile	Asn	Asn	Ala	Gly	Val	Met	Arg	Cys	Pro	His	Trp	Thr	Thr	125	130	135	
Glu	Asp	Gly	Phe	Glu	Met	Gln	Phe	Gly	Val	Asn	His	Leu	Gly	His	140	145	150	
Phe	Leu	Leu	Thr	Asn	Leu	Leu	Leu	Asp	Lys	Leu	Lys	Ala	Ser	Ala	155	160	165	
Pro	Ser	Arg	Ile	Ile	Asn	Leu	Ser	Ser	Leu	Ala	His	Val	Ala	Gly	170	175	180	

His	Ile	Asp	Phe	Asp	Asp	Leu	Asn	Trp	Gln	Thr	Arg	Lys	Tyr	Asn
				185					190					195
Thr	Lys	Ala	Ala	Tyr	Cys	Gln	Ser	Lys	Leu	Ala	Ile	Val	Leu	Phe
				200					205					210
Thr	Lys	Glu	Leu	Ser	Arg	Arg	Leu	Gln	Gly	Ser	Gly	Val	Thr	Val
				215					220					225
Asn	Ala	Leu	His	Pro	Gly	Val	Ala	Arg	Thr	Glu	Leu	Gly	Arg	His
				230					235					240
Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro
				245					250					255
Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro
				260					265					270
Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly
				275					280					285
Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala
				290					295					300
Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg
				305					310					315
Leu	Val	Gly	Leu	Glu	Ala	Pro	Ser	Val	Arg	Glu	Gln	Pro	Leu	Pro
				320					325					330

Arg

<210> 117
 <211> 2249
 <212> DNA
 <213> Homo sapiens

<400> 117
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 gggcgacacg ttctcggcgc tgaccagcgt ggcgcgcgcc ctggcgcccc 150
 agcgccggct gctggggctg ctgaggcgtt acctgcgcgg ggaggaggcg 200
 cggctgcggg acctgactag attctacgac aaggtacttt ctttgcattga 250
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 aacgcctgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350
 gagaacatcc gagctctgaa ggatggctat gagaaggtgg agcaagacct 400
 tccagccttt gaggaccttg agggagcagc aagggccctg atgcggctgc 450

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<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

Met	Gly	Pro	Gly	Ala	Arg	Leu	Ala	Ala	Leu	Leu	Ala	Val	Leu	Ala
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Leu	Gly	Thr	Gly	Asp	Pro	Glu	Arg	Ala	Ala	Ala	Arg	Gly	Asp	Thr
				20					25				30	

Phe	Ser	Ala	Leu	Thr	Ser	Val	Ala	Arg	Ala	Leu	Ala	Pro	Glu	Arg
				35					40				45	

Arg	Leu	Leu	Gly	Leu	Leu	Arg	Arg	Tyr	Leu	Arg	Gly	Glu	Glu	Ala
				50					55				60	

Arg	Leu	Arg	Asp	Leu	Thr	Arg	Phe	Tyr	Asp	Lys	Val	Leu	Ser	Leu
				65					70				75	

His	Glu	Asp	Ser	Thr	Thr	Pro	Val	Ala	Asn	Pro	Leu	Leu	Ala	Phe
				80					85				90	

Thr	Leu	Ile	Lys	Arg	Leu	Gln	Ser	Asp	Trp	Arg	Asn	Val	Val	His
				95					100				105	

Ser	Leu	Glu	Ala	Ser	Glu	Asn	Ile	Arg	Ala	Leu	Lys	Asp	Gly	Tyr
				110					115				120	

Glu	Lys	Val	Glu	Gln	Asp	Leu	Pro	Ala	Phe	Glu	Asp	Leu	Glu	Gly
				125					130				135	

Ala	Ala	Arg	Ala	Leu	Met	Arg	Leu	Gln	Asp	Val	Tyr	Met	Leu	Asn
				140					145				150	

Val	Lys	Gly	Leu	Ala	Arg	Gly	Val	Phe	Gln	Arg	Val	Thr	Gly	Ser
				155					160				165	

Ala	Ile	Thr	Asp	Leu	Tyr	Ser	Pro	Lys	Arg	Leu	Phe	Ser	Leu	Thr
				170					175				180	

Gly Asp Asp Cys	Phe Gln Val Gly Lys	Val Ala Tyr Asp Met	Gly
185	190		195
Asp Tyr Tyr His	Ala Ile Pro Trp Leu	Glu Glu Ala Val Ser	Leu
200	205		210
Phe Arg Gly Ser	Tyr Gly Glu Trp Lys	Thr Glu Asp Glu Ala	Ser
215	220		225
Leu Glu Asp Ala	Leu Asp His Leu Ala	Phe Ala Tyr Phe Arg	Ala
230	235		240
Gly Asn Val Ser	Cys Ala Leu Ser Leu	Ser Arg Glu Phe Leu	Leu
245	250		255
Tyr Ser Pro Asp	Asn Lys Arg Met Ala	Arg Asn Val Leu Lys	Tyr
260	265		270
Glu Arg Leu Leu	Ala Glu Ser Pro Asn	His Val Val Ala Glu	Ala
275	280		285
Val Ile Gln Arg	Pro Asn Ile Pro His	Leu Gln Thr Arg Asp	Thr
290	295		300
Tyr Glu Gly Leu	Cys Gln Thr Leu Gly	Ser Gln Pro Thr Leu	Tyr
305	310		315
Gln Ile Pro Ser	Leu Tyr Cys Ser Tyr	Glu Thr Asn Ser Asn	Ala
320	325		330
Tyr Leu Leu Leu	Gln Pro Ile Arg Lys	Glu Val Ile His Leu	Glu
335	340		345
Pro Tyr Ile Ala	Leu Tyr His Asp Phe	Val Ser Asp Ser Glu	Ala
350	355		360
Gln Lys Ile Arg	Glu Leu Ala Glu Pro	Trp Leu Gln Arg Ser	Val
365	370		375
Val Ala Ser Gly	Glu Lys Gln Leu Gln	Val Glu Tyr Arg Ile	Ser
380	385		390
Lys Ser Ala Trp	Leu Lys Asp Thr Val	Asp Pro Lys Leu Val	Thr
395	400		405
Leu Asn His Arg	Ile Ala Ala Leu Thr	Gly Leu Asp Val Arg	Pro
410	415		420
Pro Tyr Ala Glu	Tyr Leu Gln Val Val	Asn Tyr Gly Ile Gly	Gly
425	430		435
His Tyr Glu Pro	His Phe Asp His Ala	Thr Ser Pro Ser Ser	Pro
440	445		450
Leu Tyr Arg Met	Lys Ser Gly Asn Arg	Val Ala Thr Phe Met	Ile
455	460		465

Tyr	Leu	Ser	Ser	Val	Glu	Ala	Gly	Gly	Ala	Thr	Ala	Phe	Ile	Tyr	
				470					475					480	
Ala	Asn	Leu	Ser	Val	Pro	Val	Val	Arg	Asn	Ala	Ala	Leu	Phe	Trp	
				485					490					495	
Trp	Asn	Leu	His	Arg	Ser	Gly	Glu	Gly	Asp	Ser	Asp	Thr	Leu	His	
				500					505					510	
Ala	Gly	Cys	Pro	Val	Leu	Val	Gly	Asp	Lys	Trp	Val	Ala	Asn	Lys	
				515					520					525	
Trp	Ile	His	Glu	Tyr	Gly	Gln	Glu	Phe	Arg	Arg	Pro	Cys	Ser	Ser	
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Ser Pro Glu Asp

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<220>
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 cgggacagga gacccagaaa ggg 23

<210> 120
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 120
 ggccaagtga tccaaggcat cttc 24

<210> 121
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 121
 ctgcgggacc tgactagatt ctacgacaag gtactttctt tgcattggg 49

<210> 122
 <211> 1778
 <212> DNA
 <213> Homo sapiens

<400> 122

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gaatcgggcc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150
ggagagcccc ggagcccccg taaccgcgc ggggagcgcc caggatgccg 200
cgcggggact cggagcaggt gcgctactgc gcgcgcttct cctacctctg 250
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ccctggtcct gtctgtgggc atctatgcag aggttgagcg gcagaaatat 350
aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcctcctcct 400
gggcgtcgtc atgttcatgg tctccttcat tgggtgtgctg gcgtccctcc 450
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<210> 123

<211> 294

<212> PRT

<213> Homo sapiens

<400> 123

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				20					25					30
Phe	Trp	Leu	Ile	Gly	Ala	Leu	Val	Leu	Ser	Val	Gly	Ile	Tyr	Ala
				35					40					45
Glu	Val	Glu	Arg	Gln	Lys	Tyr	Lys	Thr	Leu	Glu	Ser	Ala	Phe	Leu
				50					55					60
Ala	Pro	Ala	Ile	Ile	Leu	Ile	Leu	Leu	Gly	Val	Val	Met	Phe	Met
				65					70					75
Val	Ser	Phe	Ile	Gly	Val	Leu	Ala	Ser	Leu	Arg	Asp	Asn	Leu	Tyr
				80					85					90
Leu	Leu	Gln	Ala	Phe	Met	Tyr	Ile	Leu	Gly	Ile	Cys	Leu	Ile	Met
				95					100					105
Glu	Leu	Ile	Gly	Gly	Val	Val	Ala	Leu	Thr	Phe	Arg	Asn	Gln	Thr
				110					115					120
Ile	Asp	Phe	Leu	Asn	Asp	Asn	Ile	Arg	Arg	Gly	Ile	Glu	Asn	Tyr
				125					130					135
Tyr	Asp	Asp	Leu	Asp	Phe	Lys	Asn	Ile	Met	Asp	Phe	Val	Gln	Lys
				140					145					150
Lys	Phe	Lys	Cys	Cys	Gly	Gly	Glu	Asp	Tyr	Arg	Asp	Trp	Ser	Lys
				155					160					165
Asn	Gln	Tyr	His	Asp	Cys	Ser	Ala	Pro	Gly	Pro	Leu	Ala	Cys	Gly

	170	175	180
Val Pro Tyr Thr Cys Cys Ile Arg Asn Thr Thr Glu Val Val Asn			
	185	190	195
Thr Met Cys Gly Tyr Lys Thr Ile Asp Lys Glu Arg Phe Ser Val			
	200	205	210
Gln Asp Val Ile Tyr Val Arg Gly Cys Thr Asn Ala Val Ile Ile			
	215	220	225
Trp Phe Met Asp Asn Tyr Thr Ile Met Ala Cys Ile Leu Leu Gly			
	230	235	240
Ile Leu Leu Pro Gln Phe Leu Gly Val Leu Leu Thr Leu Leu Tyr			
	245	250	255
Ile Thr Arg Val Glu Asp Ile Ile Met Glu His Ser Val Thr Asp			
	260	265	270
Gly Leu Leu Gly Pro Gly Ala Lys Pro Ser Val Glu Ala Ala Gly			
	275	280	285
Thr Gly Cys Cys Leu Cys Tyr Pro Asn			
	290		

<210> 124
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 124
 atcatctatt ccaccgtgtt ctggc 25

<210> 125
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 125
 gacagagtgc tccatgatga tgtcc 25

<210> 126
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 126

cctgtctgtg ggcatttatg cagaggttga gcggcagaaa tataaaaccc 50

<210> 127

<211> 1636

<212> DNA

<213> Homo sapiens

<400> 127

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ctctgtggtt tgctggcagc caccttgatc caagccaccc tcagtccac 150
tgcagttctc atcctcggcc caaaagtcac caaagaaaag ctgacacagg 200
agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc 250
agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300
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gtcaagatcc ccctggacat ggtggctgga ttcaacacgc ccctgggtcaa 450
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<210> 128

<211> 484

<212> PRT

<213> Homo sapiens

<400> 128

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Ala	Thr	Leu	Ile	Gln	Ala	Thr	Leu	Ser	Pro	Thr	Ala	Val	Leu	Ile
			20						25					30

Leu	Gly	Pro	Lys	Val	Ile	Lys	Glu	Lys	Leu	Thr	Gln	Glu	Leu	Lys
			35						40					45

Asp	His	Asn	Ala	Thr	Ser	Ile	Leu	Gln	Gln	Leu	Pro	Leu	Leu	Ser
			50						55					60

Ala	Met	Arg	Glu	Lys	Pro	Ala	Gly	Gly	Ile	Pro	Val	Leu	Gly	Ser
			65						70					75

Leu	Val	Asn	Thr	Val	Leu	Lys	His	Ile	Ile	Trp	Leu	Lys	Val	Ile
			80						85					90

Thr	Ala	Asn	Ile	Leu	Gln	Leu	Gln	Val	Lys	Pro	Ser	Ala	Asn	Asp
			95						100					105

Gln	Glu	Leu	Leu	Val	Lys	Ile	Pro	Leu	Asp	Met	Val	Ala	Gly	Phe
			110						115					120

Asn	Thr	Pro	Leu	Val	Lys	Thr	Ile	Val	Glu	Phe	His	Met	Thr	Thr
			125						130					135

Glu	Ala	Gln	Ala	Thr	Ile	Arg	Met	Asp	Thr	Ser	Ala	Ser	Gly	Pro
			140						145					150

Thr	Arg	Leu	Val	Leu	Ser	Asp	Cys	Ala	Thr	Ser	His	Gly	Ser	Leu
			155						160					165

Arg Ile Gln Leu Leu Tyr Lys Leu Ser Phe Leu Val Asn Ala Leu

	170		175		180
Ala Lys Gln Val	Met Asn Leu Leu Val	Pro Ser Leu Pro Asn	Leu		
	185		190		195
Val Lys Asn Gln	Leu Cys Pro Val Ile	Glu Ala Ser Phe Asn	Gly		
	200		205		210
Met Tyr Ala Asp	Leu Leu Gln Leu Val	Lys Val Pro Ile Ser	Leu		
	215		220		225
Ser Ile Asp Arg	Leu Glu Phe Asp Leu	Leu Tyr Pro Ala Ile	Lys		
	230		235		240
Gly Asp Thr Ile	Gln Leu Tyr Leu Gly	Ala Lys Leu Leu Asp	Ser		
	245		250		255
Gln Gly Lys Val	Thr Lys Trp Phe Asn	Asn Ser Ala Ala Ser	Leu		
	260		265		270
Thr Met Pro Thr	Leu Asp Asn Ile Pro	Phe Ser Leu Ile Val	Ser		
	275		280		285
Gln Asp Val Val	Lys Ala Ala Val Ala	Ala Val Leu Ser Pro	Glu		
	290		295		300
Glu Phe Met Val	Leu Leu Asp Ser Val	Leu Pro Glu Ser Ala	His		
	305		310		315
Arg Leu Lys Ser	Ser Ile Gly Leu Ile	Asn Glu Lys Ala Ala	Asp		
	320		325		330
Lys Leu Gly Ser	Thr Gln Ile Val Lys	Ile Leu Thr Gln Asp	Thr		
	335		340		345
Pro Glu Phe Phe	Ile Asp Gln Gly His	Ala Lys Val Ala Gln	Leu		
	350		355		360
Ile Val Leu Glu	Val Phe Pro Ser Ser	Glu Ala Leu Arg Pro	Leu		
	365		370		375
Phe Thr Leu Gly	Ile Glu Ala Ser Ser	Glu Ala Gln Phe Tyr	Thr		
	380		385		390
Lys Gly Asp Gln	Leu Ile Leu Asn Leu	Asn Asn Ile Ser Ser	Asp		
	395		400		405
Arg Ile Gln Leu	Met Asn Ser Gly Ile	Gly Trp Phe Gln Pro	Asp		
	410		415		420
Val Leu Lys Asn	Ile Ile Thr Glu Ile	Ile His Ser Ile Leu	Leu		
	425		430		435
Pro Asn Gln Asn	Gly Lys Leu Arg Ser	Gly Val Pro Val Ser	Leu		
	440		445		450
Val Lys Ala Leu	Gly Phe Glu Ala Ala	Glu Ser Ser Leu Thr	Lys		

455	460	465
Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser		
470	475	480

Pro Val Ser Gln

<210> 129
 <211> 2213
 <212> DNA
 <213> Homo sapiens

<400> 129
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<210> 130

<211> 335

<212> PRT

<213> Homo sapiens

<400> 130

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Arg	Lys	Lys	Glu	Met	Val	Leu	Ser	Glu	Lys	Val	Ser	Gln	Leu	Met					
35										40					45				
Glu	Trp	Thr	Asn	Lys	Arg	Pro	Val	Ile	Arg	Met	Asn	Gly	Asp	Lys					
50										55					60				
Phe	Arg	Arg	Leu	Val	Lys	Ala	Pro	Pro	Arg	Asn	Tyr	Ser	Val	Ile					
65										70					75				
Val	Met	Phe	Thr	Ala	Leu	Gln	Leu	His	Arg	Gln	Cys	Val	Val	Cys					
80										85					90				
Lys	Gln	Ala	Asp	Glu	Glu	Phe	Gln	Ile	Leu	Ala	Asn	Ser	Trp	Arg					
95										100					105				
Tyr	Ser	Ser	Ala	Phe	Thr	Asn	Arg	Ile	Phe	Phe	Ala	Met	Val	Asp					
110										115					120				
Phe	Asp	Glu	Gly	Ser	Asp	Val	Phe	Gln	Met	Leu	Asn	Met	Asn	Ser					
125										130					135				
Ala	Pro	Thr	Phe	Ile	Asn	Phe	Pro	Ala	Lys	Gly	Lys	Pro	Lys	Arg					
140										145					150				
Gly	Asp	Thr	Tyr	Glu	Leu	Gln	Val	Arg	Gly	Phe	Ser	Ala	Glu	Gln					
155										160					165				
Ile	Ala	Arg	Trp	Ile	Ala	Asp	Arg	Thr	Asp	Val	Asn	Ile	Arg	Val					
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Ile	Arg	Pro	Pro	Asn	Tyr	Ala	Gly	Pro	Leu	Met	Leu	Gly	Leu	Leu					
185										190					195				
Leu	Ala	Val	Ile	Gly	Gly	Leu	Val	Tyr	Leu	Arg	Arg	Ser	Asn	Met					
200										205					210				
Glu	Phe	Leu	Phe	Asn	Lys	Thr	Gly	Trp	Ala	Phe	Ala	Ala	Leu	Cys					
215										220					225				
Phe	Val	Leu	Ala	Met	Thr	Ser	Gly	Gln	Met	Trp	Asn	His	Ile	Arg					
230										235					240				
Gly	Pro	Pro	Tyr	Ala	His	Lys	Asn	Pro	His	Thr	Gly	His	Val	Asn					
245										250					255				
Tyr	Ile	His	Gly	Ser	Ser	Gln	Ala	Gln	Phe	Val	Ala	Glu	Thr	His					
260										265					270				
Ile	Val	Leu	Leu	Phe	Asn	Gly	Gly	Val	Thr	Leu	Gly	Met	Val	Leu					
275										280					285				
Leu	Cys	Glu	Ala	Ala	Thr	Ser	Asp	Met	Asp	Ile	Gly	Lys	Arg	Lys					
290										295					300				
Ile	Met	Cys	Val	Ala	Gly	Ile	Gly	Leu	Val	Val	Leu	Phe	Phe	Ser					

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Ser Phe Leu Met Ser					
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<210> 131

<211> 2476

<212> DNA

<213> Homo sapiens

<400> 131

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cttggcgctg gcggtactgg ccccgaggagc aggggagcag aggcggagag 200
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<210> 132
 <211> 536
 <212> PRT
 <213> Homo sapiens

<400> 132

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Val	Leu	Ala	Pro	Gly	Ala	Gly	Glu	Gln	Arg	Arg	Arg	Ala	Ala	Lys	
				20					25					30	
Ala	Pro	Asn	Val	Val	Leu	Val	Val	Ser	Asp	Ser	Phe	Asp	Gly	Arg	
				35					40					45	
Leu	Thr	Phe	His	Pro	Gly	Ser	Gln	Val	Val	Lys	Leu	Pro	Phe	Ile	
				50					55					60	
Asn	Phe	Met	Lys	Thr	Arg	Gly	Thr	Ser	Phe	Leu	Asn	Ala	Tyr	Thr	
				65					70					75	
Asn	Ser	Pro	Ile	Cys	Cys	Pro	Ser	Arg	Ala	Ala	Met	Trp	Ser	Gly	
				80					85					90	
Leu	Phe	Thr	His	Leu	Thr	Glu	Ser	Trp	Asn	Asn	Phe	Lys	Gly	Leu	
				95					100					105	
Asp	Pro	Asn	Tyr	Thr	Thr	Trp	Met	Asp	Val	Met	Glu	Arg	His	Gly	
				110					115					120	
Tyr	Arg	Thr	Gln	Lys	Phe	Gly	Lys	Leu	Asp	Tyr	Thr	Ser	Gly	His	
				125					130					135	
His	Ser	Ile	Ser	Asn	Arg	Val	Glu	Ala	Trp	Thr	Arg	Asp	Val	Ala	
				140					145					150	
Phe	Leu	Leu	Arg	Gln	Glu	Gly	Arg	Pro	Met	Val	Asn	Leu	Ile	Arg	
				155					160					165	
Asn	Arg	Thr	Lys	Val	Arg	Val	Met	Glu	Arg	Asp	Trp	Gln	Asn	Thr	
				170					175					180	
Asp	Lys	Ala	Val	Asn	Trp	Leu	Arg	Lys	Glu	Ala	Ile	Asn	Tyr	Thr	
				185					190					195	
Glu	Pro	Phe	Val	Ile	Tyr	Leu	Gly	Leu	Asn	Leu	Pro	His	Pro	Tyr	
				200					205					210	
Pro	Ser	Pro	Ser	Ser	Gly	Glu	Asn	Phe	Gly	Ser	Ser	Thr	Phe	His	
				215					220					225	
Thr	Ser	Leu	Tyr	Trp	Leu	Glu	Lys	Val	Ser	His	Asp	Ala	Ile	Lys	
				230					235					240	
Ile	Pro	Lys	Trp	Ser	Pro	Leu	Ser	Glu	Met	His	Pro	Val	Asp	Tyr	
				245					250					255	

Tyr Ser Ser Tyr	Thr Lys Asn Cys Thr	Gly Arg Phe Thr Lys Lys	260	265	270
Glu Ile Lys Asn	Ile Arg Ala Phe Tyr	Tyr Ala Met Cys Ala Glu	275	280	285
Thr Asp Ala Met	Leu Gly Glu Ile Ile	Leu Ala Leu His Gln Leu	290	295	300
Asp Leu Leu Gln	Lys Thr Ile Val Ile	Tyr Ser Ser Asp His Gly	305	310	315
Glu Leu Ala Met	Glu His Arg Gln Phe	Tyr Lys Met Ser Met Tyr	320	325	330
Glu Ala Ser Ala	His Val Pro Leu Leu	Met Met Gly Pro Gly Ile	335	340	345
Lys Ala Gly Leu	Gln Val Ser Asn Val	Val Ser Leu Val Asp Ile	350	355	360
Tyr Pro Thr Met	Leu Asp Ile Ala Gly	Ile Pro Leu Pro Gln Asn	365	370	375
Leu Ser Gly Tyr	Ser Leu Leu Pro Leu	Ser Ser Glu Thr Phe Lys	380	385	390
Asn Glu His Lys	Val Lys Asn Leu His	Pro Pro Trp Ile Leu Ser	395	400	405
Glu Phe His Gly	Cys Asn Val Asn Ala	Ser Thr Tyr Met Leu Arg	410	415	420
Thr Asn His Trp	Lys Tyr Ile Ala Tyr	Ser Asp Gly Ala Ser Ile	425	430	435
Leu Pro Gln Leu	Phe Asp Leu Ser Ser	Asp Pro Asp Glu Leu Thr	440	445	450
Asn Val Ala Val	Lys Phe Pro Glu Ile	Thr Tyr Ser Leu Asp Gln	455	460	465
Lys Leu His Ser	Ile Ile Asn Tyr Pro	Lys Val Ser Ala Ser Val	470	475	480
His Gln Tyr Asn	Lys Glu Gln Phe Ile	Lys Trp Lys Gln Ser Ile	485	490	495
Gly Gln Asn Tyr	Ser Asn Val Ile Ala	Asn Leu Arg Trp His Gln	500	505	510
Asp Trp Gln Lys	Glu Pro Arg Lys Tyr	Glu Asn Ala Ile Asp Gln	515	520	525
Trp Leu Lys Thr	His Met Asn Pro Arg	Ala Val	530	535	

<210> 133
<211> 1475
<212> DNA
<213> Homo sapiens

<400> 133
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ctacatccta ggccttcttg ggcttttggg cacactgggt gccatgctgc 200
tccccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250
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<210> 134
 <211> 230
 <212> PRT
 <213> Homo sapiens

<400> 134

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Leu	Gly	Leu	Leu	Gly	Thr	Leu	Val	Ala	Met	Leu	Leu	Pro	Ser	Trp	20	25	30	
Lys	Thr	Ser	Ser	Tyr	Val	Gly	Ala	Ser	Ile	Val	Thr	Ala	Val	Gly	35	40	45	
Phe	Ser	Lys	Gly	Leu	Trp	Met	Glu	Cys	Ala	Thr	His	Ser	Thr	Gly	50	55	60	
Ile	Thr	Gln	Cys	Asp	Ile	Tyr	Ser	Thr	Leu	Leu	Gly	Leu	Pro	Ala	65	70	75	
Asp	Ile	Gln	Ala	Ala	Gln	Ala	Met	Met	Val	Thr	Ser	Ser	Ala	Ile	80	85	90	
Ser	Ser	Leu	Ala	Cys	Ile	Ile	Ser	Val	Val	Gly	Met	Arg	Cys	Thr	95	100	105	
Val	Phe	Cys	Gln	Glu	Ser	Arg	Ala	Lys	Asp	Arg	Val	Ala	Val	Ala	110	115	120	
Gly	Gly	Val	Phe	Phe	Ile	Leu	Gly	Gly	Leu	Leu	Gly	Phe	Ile	Pro	125	130	135	
Val	Ala	Trp	Asn	Leu	His	Gly	Ile	Leu	Arg	Asp	Phe	Tyr	Ser	Pro	140	145	150	
Leu	Val	Pro	Asp	Ser	Met	Lys	Phe	Glu	Ile	Gly	Glu	Ala	Leu	Tyr	155	160	165	
Leu	Gly	Ile	Ile	Ser	Ser	Leu	Phe	Ser	Leu	Ile	Ala	Gly	Ile	Ile	170	175	180	
Leu	Cys	Phe	Ser	Cys	Ser	Ser	Gln	Arg	Asn	Arg	Ser	Asn	Tyr	Tyr	185	190	195	
Asp	Ala	Tyr	Gln	Ala	Gln	Pro	Leu	Ala	Thr	Arg	Ser	Ser	Pro	Arg	200	205	210	

Pro Gly Gln Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser
 215 220 225

Leu Thr Gly Tyr Val
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<210> 135

<211> 610

<212> DNA

<213> Homo sapiens

<400> 135

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 acctgtaaaa 610

<210> 136

<211> 119

<212> PRT

<213> Homo sapiens

<400> 136

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 Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu
 20 25 30
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
 35 40 45
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
 50 55 60
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys

	65		70		75									
Phe	Glu	Leu	Cys	Cys	Leu	Asp	Ser	Phe	Gly	Leu	Thr	Asn	Asp	Phe
			80						85					90
Val	Val	Lys	Leu	Lys	Val	Gln	Gly	Val	Asn	Ser	Gln	Cys	His	Ser
			95						100					105
Ser	Pro	Ile	Ser	Ser	Lys	Cys	Glu	Ser	Arg	Arg	Arg	Phe	Pro	
			110						115					

<210> 137
 <211> 771
 <212> DNA
 <213> Homo sapiens

<400> 137
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<210> 138
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 138
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 1 5 10 15

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				20					25					30	
Thr	Pro	Tyr	Leu	Met	Leu	Cys	Gln	Pro	His	Lys	Arg	Cys	Gly	Asp	
				35					40					45	
Lys	Phe	Tyr	Asp	Pro	Leu	Gln	His	Cys	Cys	Tyr	Asp	Asp	Ala	Val	
				50					55					60	
Val	Pro	Leu	Ala	Arg	Thr	Gln	Thr	Cys	Gly	Asn	Cys	Thr	Phe	Arg	
				65					70					75	
Val	Cys	Phe	Glu	Gln	Cys	Cys	Pro	Trp	Thr	Phe	Met	Val	Lys	Leu	
				80					85					90	
Ile	Asn	Gln	Asn	Cys	Asp	Ser	Ala	Arg	Thr	Ser	Asp	Asp	Arg	Leu	
				95					100					105	
Cys	Arg	Ser	Val	Ser											
				110											

<210> 139

<211> 2044

<212> DNA

<213> Homo sapiens

<400> 139

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<210> 140

<211> 311

<212> PRT

<213> Homo sapiens

<400> 140

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				20					25					30	
Ala	Ala	Phe	Lys	Val	Ala	Thr	Pro	Tyr	Ser	Leu	Tyr	Val	Cys	Pro	
				35					40					45	
Glu	Gly	Gln	Asn	Val	Thr	Leu	Thr	Cys	Arg	Leu	Leu	Gly	Pro	Val	
				50					55					60	
Asp	Lys	Gly	His	Asp	Val	Thr	Phe	Tyr	Lys	Thr	Trp	Tyr	Arg	Ser	
				65					70					75	
Ser	Arg	Gly	Glu	Val	Gln	Thr	Cys	Ser	Glu	Arg	Arg	Pro	Ile	Arg	
				80					85					90	
Asn	Leu	Thr	Phe	Gln	Asp	Leu	His	Leu	His	His	Gly	Gly	His	Gln	
				95					100					105	
Ala	Ala	Asn	Thr	Ser	His	Asp	Leu	Ala	Gln	Arg	His	Gly	Leu	Glu	
				110					115					120	
Ser	Ala	Ser	Asp	His	His	Gly	Asn	Phe	Ser	Ile	Thr	Met	Arg	Asn	
				125					130					135	
Leu	Thr	Leu	Leu	Asp	Ser	Gly	Leu	Tyr	Cys	Cys	Leu	Val	Val	Glu	
				140					145					150	
Ile	Arg	His	His	His	Ser	Glu	His	Arg	Val	His	Gly	Ala	Met	Glu	
				155					160					165	
Leu	Gln	Val	Gln	Thr	Gly	Lys	Asp	Ala	Pro	Ser	Asn	Cys	Val	Val	
				170					175					180	
Tyr	Pro	Ser	Ser	Ser	Gln	Asp	Ser	Glu	Asn	Ile	Thr	Ala	Ala	Ala	
				185					190					195	
Leu	Ala	Thr	Gly	Ala	Cys	Ile	Val	Gly	Ile	Leu	Cys	Leu	Pro	Leu	
				200					205					210	
Ile	Leu	Leu	Leu	Val	Tyr	Lys	Gln	Arg	Gln	Ala	Ala	Ser	Asn	Arg	
				215					220					225	
Arg	Ala	Gln	Glu	Leu	Val	Arg	Met	Asp	Ser	Asn	Ile	Gln	Gly	Ile	
				230					235					240	
Glu	Asn	Pro	Gly	Phe	Glu	Ala	Ser	Pro	Pro	Ala	Gln	Gly	Ile	Pro	
				245					250					255	
Glu	Ala	Lys	Val	Arg	His	Pro	Leu	Ser	Tyr	Val	Ala	Gln	Arg	Gln	
				260					265					270	
Pro	Ser	Glu	Ser	Gly	Arg	His	Leu	Leu	Ser	Glu	Pro	Ser	Thr	Pro	

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Leu Ser Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp					
	290		295		300
Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile					
	305		310		

<210> 141
 <211> 1732
 <212> DNA
 <213> Homo sapiens

<400> 141
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 cttagacctc ctttctgccc ctcttttctt gccaccgct gcttcttggc 150
 ctttctccga ccccgctcta gcagcagacc tcttgggggc tgtgggttga 200
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 ccgctcccg accagcggcc tgacctggg gaaaggatgg ttcccgaggt 300
 gagggctctc tcttcttgc tgggactcgc gctgctctgg ttccccctgg 350
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 agatactccc ccggcgagag ctggcacccc tacttgagc cacaaggcct 450
 gatgtactgc ctgcgctgta cctgctcaga gggcgcccat gtgagttgtt 500
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 aagcctgcaa agatgaggca agtgagcaat cggatgaaga ggacagtgtg 850
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 cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732

<210> 142
 <211> 451
 <212> PRT
 <213> Homo sapiens

<400> 142
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 20 25 30
 Met Phe Cys Leu Phe His Gly Lys Arg Tyr Ser Pro Gly Glu Ser
 35 40 45
 Trp His Pro Tyr Leu Glu Pro Gln Gly Leu Met Tyr Cys Leu Arg
 50 55 60
 Cys Thr Cys Ser Glu Gly Ala His Val Ser Cys Tyr Arg Leu His
 65 70 75
 Cys Pro Pro Val His Cys Pro Gln Pro Val Thr Glu Pro Gln Gln
 80 85 90
 Cys Cys Pro Lys Cys Val Glu Pro His Thr Pro Ser Gly Leu Arg
 95 100 105
 Ala Pro Pro Lys Ser Cys Gln His Asn Gly Thr Met Tyr Gln His
 110 115 120

Gly	Glu	Ile	Phe	Ser	Ala	His	Glu	Leu	Phe	Pro	Ser	Arg	Leu	Pro	125	130	135
Asn	Gln	Cys	Val	Leu	Cys	Ser	Cys	Thr	Glu	Gly	Gln	Ile	Tyr	Cys	140	145	150
Gly	Leu	Thr	Thr	Cys	Pro	Glu	Pro	Gly	Cys	Pro	Ala	Pro	Leu	Pro	155	160	165
Leu	Pro	Asp	Ser	Cys	Cys	Gln	Ala	Cys	Lys	Asp	Glu	Ala	Ser	Glu	170	175	180
Gln	Ser	Asp	Glu	Glu	Asp	Ser	Val	Gln	Ser	Leu	His	Gly	Val	Arg	185	190	195
His	Pro	Gln	Asp	Pro	Cys	Ser	Ser	Asp	Ala	Gly	Arg	Lys	Arg	Gly	200	205	210
Pro	Gly	Thr	Pro	Ala	Pro	Thr	Gly	Leu	Ser	Ala	Pro	Leu	Ser	Phe	215	220	225
Ile	Pro	Arg	His	Phe	Arg	Pro	Lys	Gly	Ala	Gly	Ser	Thr	Thr	Val	230	235	240
Lys	Ile	Val	Leu	Lys	Glu	Lys	His	Lys	Lys	Ala	Cys	Val	His	Gly	245	250	255
Gly	Lys	Thr	Tyr	Ser	His	Gly	Glu	Val	Trp	His	Pro	Ala	Phe	Arg	260	265	270
Ala	Phe	Gly	Pro	Leu	Pro	Cys	Ile	Leu	Cys	Thr	Cys	Glu	Asp	Gly	275	280	285
Arg	Gln	Asp	Cys	Gln	Arg	Val	Thr	Cys	Pro	Thr	Glu	Tyr	Pro	Cys	290	295	300
Arg	His	Pro	Glu	Lys	Val	Ala	Gly	Lys	Cys	Cys	Lys	Ile	Cys	Pro	305	310	315
Glu	Asp	Lys	Ala	Asp	Pro	Gly	His	Ser	Glu	Ile	Ser	Ser	Thr	Arg	320	325	330
Cys	Pro	Lys	Ala	Pro	Gly	Arg	Val	Leu	Val	His	Thr	Ser	Val	Ser	335	340	345
Pro	Ser	Pro	Asp	Asn	Leu	Arg	Arg	Phe	Ala	Leu	Glu	His	Glu	Ala	350	355	360
Ser	Asp	Leu	Val	Glu	Ile	Tyr	Leu	Trp	Lys	Leu	Val	Lys	Asp	Glu	365	370	375
Glu	Thr	Glu	Ala	Gln	Arg	Gly	Glu	Val	Pro	Gly	Pro	Arg	Pro	His	380	385	390
Ser	Gln	Asn	Leu	Pro	Leu	Asp	Ser	Asp	Gln	Glu	Ser	Gln	Glu	Ala	395	400	405

Arg Leu Pro Glu Arg Gly Thr Ala Leu Pro Thr Ala Arg Trp Pro
 410 415 420

Pro Arg Arg Ser Leu Glu Arg Leu Pro Ser Pro Asp Pro Gly Ala
 425 430 435

Glu Gly His Gly Gln Ser Arg Gln Ser Asp Gln Asp Ile Thr Lys
 440 445 450

Thr

<210> 143
 <211> 693
 <212> DNA
 <213> Homo sapiens

<400> 143
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 cttgcggaaa atgctgatct cagtcgcaat gctgggcgca ggggctggcg 150
 tgggctacgc gtcctcgtt atcgtgaccc cgggagagcg gcggaagcag 200
 gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250
 ggccaggacc cagcagctat tgctggccac tctgcaggag gcagcgacca 300
 cgcaggagaa cgtggcctgg aggaagaact ggatggttgg cggcgaaggc 350
 ggcgccagcg ggaggtcacc gtgagaccgg acttgcctcc gtgggcgcgcg 400
 gaccttggct tgggcgcagg aatccgaggc agcctttctc cttcgtgggc 450
 ccagcggaga gtccggaccg agataccatg ccaggactct ccggggctct 500
 gtgagctgcc gtcgggtgag cacgtttccc ccaaaccctg gactgactgc 550
 tttaaggtcc gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600
 aactgaaaga accaataaaa tcatgttcct ccaaaaaaaaaa aaaaaaaaaa 650
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 144
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 1 5 10 15
 Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro
 20 25 30

Gly	Glu	Arg	Arg	Lys	Gln	Glu	Met	Leu	Lys	Glu	Met	Pro	Leu	Gln
				35					40					45
Asp	Pro	Arg	Ser	Arg	Glu	Glu	Ala	Ala	Arg	Thr	Gln	Gln	Leu	Leu
				50					55					60
Leu	Ala	Thr	Leu	Gln	Glu	Ala	Ala	Thr	Thr	Gln	Glu	Asn	Val	Ala
				65					70					75
Trp	Arg	Lys	Asn	Trp	Met	Val	Gly	Gly	Glu	Gly	Gly	Ala	Ser	Gly
				80					85					90
Arg Ser Pro														

<210> 145

<211> 1883

<212> DNA

<213> Homo sapiens

<400> 145

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caggctgcca tggggccag caccctctc ctcatcttgt tccttttgtc 150
atggtcggga cccctccaag gacagcagca ccaccttggt gagtacatgg 200
aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250
agtagtcggc atgctgctga gctgcgggac ttcaagaaca agatgctgcc 300
actgctggag gtggcagaga aggagcggga ggcactcaga actgaggccg 350
acaccatctc cgggagagtg gatcgtctgg agcgggaggt agactatctg 400
gagaccaga acccagctct gccctgtgta gagtttgatg agaaggtgac 450
tggaggccct gggaccaaag gcaagggaag aaggaatgag aagtacgata 500
tggtgacaga ctgtggctac acaatctctc aagtgagatc aatgaagatt 550
ctgaagcgat ttggtggccc agctggtcta tggaccaagg atccactggg 600
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aaccgaacag tgggtggacag ctcagtattc ccagcagagg ggctgatccc 900

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ccccacggc ttgacagcag acacctacat cgacctggta gctgatgagg 950
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accatgtccc agagagaatg ctgaggctgc ctttgtcatc tgtgggaccc 1100
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aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1883

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<210> 146

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

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Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp
 1             5             10             15

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```

Ser Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met
          20             25             30

```

```

Glu Arg Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln
          35             40             45

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Asp Gln Ser Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn

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50										55					60				
Lys	Met	Leu	Pro	Leu	Leu	Glu	Val	Ala	Glu	Lys	Glu	Arg	Glu	Ala					
				65					70					75					
Leu	Arg	Thr	Glu	Ala	Asp	Thr	Ile	Ser	Gly	Arg	Val	Asp	Arg	Leu					
				80					85					90					
Glu	Arg	Glu	Val	Asp	Tyr	Leu	Glu	Thr	Gln	Asn	Pro	Ala	Leu	Pro					
				95					100					105					
Cys	Val	Glu	Phe	Asp	Glu	Lys	Val	Thr	Gly	Gly	Pro	Gly	Thr	Lys					
				110					115					120					
Gly	Lys	Gly	Arg	Arg	Asn	Glu	Lys	Tyr	Asp	Met	Val	Thr	Asp	Cys					
				125					130					135					
Gly	Tyr	Thr	Ile	Ser	Gln	Val	Arg	Ser	Met	Lys	Ile	Leu	Lys	Arg					
				140					145					150					
Phe	Gly	Gly	Pro	Ala	Gly	Leu	Trp	Thr	Lys	Asp	Pro	Leu	Gly	Gln					
				155					160					165					
Thr	Glu	Lys	Ile	Tyr	Val	Leu	Asp	Gly	Thr	Gln	Asn	Asp	Thr	Ala					
				170					175					180					
Phe	Val	Phe	Pro	Arg	Leu	Arg	Asp	Phe	Thr	Leu	Ala	Met	Ala	Ala					
				185					190					195					
Arg	Lys	Ala	Ser	Arg	Val	Arg	Val	Pro	Phe	Pro	Trp	Val	Gly	Thr					
				200					205					210					
Gly	Gln	Leu	Val	Tyr	Gly	Gly	Phe	Leu	Tyr	Phe	Ala	Arg	Arg	Pro					
				215					220					225					
Pro	Gly	Arg	Pro	Gly	Gly	Gly	Gly	Glu	Met	Glu	Asn	Thr	Leu	Gln					
				230					235					240					
Leu	Ile	Lys	Phe	His	Leu	Ala	Asn	Arg	Thr	Val	Val	Asp	Ser	Ser					
				245					250					255					
Val	Phe	Pro	Ala	Glu	Gly	Leu	Ile	Pro	Pro	Tyr	Gly	Leu	Thr	Ala					
				260					265					270					
Asp	Thr	Tyr	Ile	Asp	Leu	Val	Ala	Asp	Glu	Glu	Gly	Leu	Trp	Ala					
				275					280					285					
Val	Tyr	Ala	Thr	Arg	Glu	Asp	Asp	Arg	His	Leu	Cys	Leu	Ala	Lys					
				290					295					300					
Leu	Asp	Pro	Gln	Thr	Leu	Asp	Thr	Glu	Gln	Gln	Trp	Asp	Thr	Pro					
				305					310					315					
Cys	Pro	Arg	Glu	Asn	Ala	Glu	Ala	Ala	Phe	Val	Ile	Cys	Gly	Thr					
				320					325					330					
Leu	Tyr	Val	Val	Tyr	Asn	Thr	Arg	Pro	Ala	Ser	Arg	Ala	Arg	Ile					

	335		340		345
Gln Cys Ser Phe	Asp Ala Ser Gly Thr	Leu Thr Pro Glu Arg	Ala		
	350	355	360		
Ala Leu Pro Tyr	Phe Pro Arg Arg Tyr	Gly Ala His Ala Ser	Leu		
	365	370	375		
Arg Tyr Asn Pro	Arg Glu Arg Gln Leu	Tyr Ala Trp Asp Asp	Gly		
	380	385	390		
Tyr Gln Ile Val	Tyr Lys Leu Glu Met	Arg Lys Lys Glu Glu	Glu		
	395	400	405		

Val

<210> 147
 <211> 2052
 <212> DNA
 <213> Homo sapiens

<400> 147
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 gttctcctct tctctctaata ccatccgtca cctctcctgt catccgtttc 150
 catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200
 ttggttctga gtctcctcaa gctgggatca gggcagtggc aggtgtttgg 250
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 aggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400
 gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450
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aa 2052

<210> 148

<211> 500

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly

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Ser Gly Gln Trp	Gln Val Phe Gly Pro	Asp Lys Pro Val Gln	Ala
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Leu Val Gly Glu	Asp Ala Ala Phe Ser	Cys Phe Leu Ser Pro	Lys
	35	40	45
Thr Asn Ala Glu	Ala Met Glu Val Arg	Phe Phe Arg Gly Gln	Phe
	50	55	60
Ser Ser Val Val	His Leu Tyr Arg Asp	Gly Lys Asp Gln Pro	Phe
	65	70	75
Met Gln Met Pro	Gln Tyr Gln Gly Arg	Thr Lys Leu Val Lys	Asp
	80	85	90
Ser Ile Ala Glu	Gly Arg Ile Ser Leu	Arg Leu Glu Asn Ile	Thr
	95	100	105
Val Leu Asp Ala	Gly Leu Tyr Gly Cys	Arg Ile Ser Ser Gln	Ser
	110	115	120
Tyr Tyr Gln Lys	Ala Ile Trp Glu Leu	Gln Val Ser Ala Leu	Gly
	125	130	135
Ser Val Pro Leu	Ile Ser Ile Thr Gly	Tyr Val Asp Arg Asp	Ile
	140	145	150
Gln Leu Leu Cys	Gln Ser Ser Gly Trp	Phe Pro Arg Pro Thr	Ala
	155	160	165
Lys Trp Lys Gly	Pro Gln Gly Gln Asp	Leu Ser Thr Asp Ser	Arg
	170	175	180
Thr Asn Arg Asp	Met His Gly Leu Phe	Asp Val Glu Ile Ser	Leu
	185	190	195
Thr Val Gln Glu	Asn Ala Gly Ser Ile	Ser Cys Ser Met Arg	His
	200	205	210
Ala His Leu Ser	Arg Glu Val Glu Ser	Arg Val Gln Ile Gly	Asp
	215	220	225
Thr Phe Phe Glu	Pro Ile Ser Trp His	Leu Ala Thr Lys Val	Leu
	230	235	240
Gly Ile Leu Cys	Cys Gly Leu Phe Phe	Gly Ile Val Gly Leu	Lys
	245	250	255
Ile Phe Phe Ser	Lys Phe Gln Trp Lys	Ile Gln Ala Glu Leu	Asp
	260	265	270
Trp Arg Arg Lys	His Gly Gln Ala Glu	Leu Arg Asp Ala Arg	Lys
	275	280	285
His Ala Val Glu	Val Thr Leu Asp Pro	Glu Thr Ala His Pro	Lys

290	295	300
Leu Cys Val Ser Asp Leu Lys Thr Val	Thr His Arg Lys Ala Pro	
305	310	315
Gln Glu Val Pro His Ser Glu Lys Arg	Phe Thr Arg Lys Ser Val	
320	325	330
Val Ala Ser Gln Ser Phe Gln Ala Gly	Lys His Tyr Trp Glu Val	
335	340	345
Asp Gly Gly His Asn Lys Arg Trp Arg	Val Gly Val Cys Arg Asp	
350	355	360
Asp Val Asp Arg Arg Lys Glu Tyr Val	Thr Leu Ser Pro Asp His	
365	370	375
Gly Tyr Trp Val Leu Arg Leu Asn Gly	Glu His Leu Tyr Phe Thr	
380	385	390
Leu Asn Pro Arg Phe Ile Ser Val Phe	Pro Arg Thr Pro Pro Thr	
395	400	405
Lys Ile Gly Val Phe Leu Asp Tyr Glu	Cys Gly Thr Ile Ser Phe	
410	415	420
Phe Asn Ile Asn Asp Gln Ser Leu Ile	Tyr Thr Leu Thr Cys Arg	
425	430	435
Phe Glu Gly Leu Leu Arg Pro Tyr Ile	Glu Tyr Pro Ser Tyr Asn	
440	445	450
Glu Gln Asn Gly Thr Pro Ile Val Ile	Cys Pro Val Thr Gln Glu	
455	460	465
Ser Glu Lys Glu Ala Ser Trp Gln Arg	Ala Ser Ala Ile Pro Glu	
470	475	480
Thr Ser Asn Ser Glu Ser Ser Ser Gln	Ala Thr Thr Pro Phe Leu	
485	490	495
Pro Arg Gly Glu Met		
500		

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 149

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<210> 150

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 150

ggaactgacc cagtgtgac acc 23

<210> 151

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 151

gcagatgccca cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152

<211> 2294

<212> DNA

<213> Homo sapiens

<400> 152

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aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctgggcg 150
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tggcccgcg cgcgaccacc ctgtagcgac caccgtaccg gcgcccacga 600
ctccccggac ccgaccccc gatctcccca gcagcagcaa cagcagcgtc 650
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tgtatgtaac tgctctgtgg ttggaagcct gaatgtgaat cgctgcaacc 750
agaccacagg gcagtgtgag tgtcgccag gttatcagg gcttcactgt 800

gaaacctgca aagagggcctt ttacctaaat tacacttctg ggctctgtca 850
gccatgtgac tgtagtccac atggagctct cagcataccg tgcaacaggt 900
aagcaacaga ggggtggaact gaagtttatt ttatttttagc aagggaaaaa 950
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<210> 153

<211> 258

<212> PRT

<213> Homo sapiens

<400> 153

Met	Arg	Ser	Leu	Pro	Ser	Leu	Gly	Gly	Leu	Ala	Leu	Leu	Cys	Cys
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Ala	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ser	Ala	Ala	Ser	Ala	Gly	Asn
				20					25					30

Val	Thr	Gly	Gly	Gly	Gly	Ala	Ala	Gly	Gln	Val	Asp	Ala	Ser	Pro
				35					40					45

Gly	Pro	Gly	Leu	Arg	Gly	Glu	Pro	Ser	His	Pro	Phe	Pro	Arg	Ala
				50					55					60

Thr	Ala	Pro	Thr	Ala	Gln	Ala	Pro	Arg	Thr	Gly	Pro	Pro	Arg	Ala
				65					70					75

Thr	Val	His	Arg	Pro	Leu	Ala	Ala	Thr	Ser	Pro	Ala	Gln	Ser	Pro
				80					85					90

Glu	Thr	Thr	Pro	Leu	Trp	Ala	Thr	Ala	Gly	Pro	Ser	Ser	Thr	Thr
				95					100					105

Phe	Gln	Ala	Pro	Leu	Gly	Pro	Ser	Pro	Thr	Thr	Pro	Pro	Ala	Ala
				110					115					120

Glu	Arg	Thr	Ser	Thr	Thr	Ser	Gln	Ala	Pro	Thr	Arg	Pro	Ala	Pro
				125					130					135

Thr	Thr	Leu	Ser	Thr	Thr	Thr	Gly	Pro	Ala	Pro	Thr	Thr	Pro	Val
				140					145					150

Ala	Thr	Thr	Val	Pro	Ala	Pro	Thr	Thr	Pro	Arg	Thr	Pro	Thr	Pro
				155					160					165

Asp	Leu	Pro	Ser	Ser	Ser	Asn	Ser	Ser	Val	Leu	Pro	Thr	Pro	Pro
				170					175					180

Ala	Thr	Glu	Ala	Pro	Ser	Ser	Pro	Pro	Pro	Glu	Tyr	Val	Cys	Asn
				185					190					195

Cys	Ser	Val	Val	Gly	Ser	Leu	Asn	Val	Asn	Arg	Cys	Asn	Gln	Thr
				200					205					210

Thr	Gly	Gln	Cys	Glu	Cys	Arg	Pro	Gly	Tyr	Gln	Gly	Leu	His	Cys
				215					220					225

Glu	Thr	Cys	Lys	Glu	Gly	Phe	Tyr	Leu	Asn	Tyr	Thr	Ser	Gly	Leu
				230					235					240

Cys	Gln	Pro	Cys	Asp	Cys	Ser	Pro	His	Gly	Ala	Leu	Ser	Ile	Pro
				245					250					255

Cys Asn Arg

<210> 154
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 154
 aactgctctg tggttggaag cctg 24

<210> 155
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 155
 cagtcacatg gctgacagac ccac 24

<210> 156
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 156
 aggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157
 <211> 689
 <212> DNA
 <213> Homo sapiens

<400> 157
 tgcggcgag tgtagacctg ggaggatggg cggcctgctg ctggctgctt 50
 ttctggcttt ggtctcggtg ccagggccc aggcctgtgt gttgggaaga 100
 ctggaccctg agcagcttct tgggccctgg tacgtgcttg cggtggcctc 150
 ccgggaaaag ggctttgcc tggagaagga catgaagaac gtcgtggggg 200
 tggtggtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250
 cacgggctgg gaggggtgtga ccagagtgtc atggacctga taaagcgaaa 300

ctccggatgg gtgtttgaga atccctcaat aggcgtgctg gagctctggg 350
 tgctggccac caacttcaga gactatgcca tcatcttcac tcagctggag 400
 ttcggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450
 agccagccag gaggccatgg ggctcttcac caagtggagc aggagcctgg 500
 gcttcctgtc acagtagcag gccagctgc agaaggacct cacctgtgct 550
 cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgccaca 600
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 gggcccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158

<211> 163

<212> PRT

<213> Homo sapiens

<400> 158

Met	Gly	Gly	Leu	Leu	Leu	Ala	Ala	Phe	Leu	Ala	Leu	Val	Ser	Val	1	5	10	15
Pro	Arg	Ala	Gln	Ala	Val	Trp	Leu	Gly	Arg	Leu	Asp	Pro	Glu	Gln	20	25	30	
Leu	Leu	Gly	Pro	Trp	Tyr	Val	Leu	Ala	Val	Ala	Ser	Arg	Glu	Lys	35	40	45	
Gly	Phe	Ala	Met	Glu	Lys	Asp	Met	Lys	Asn	Val	Val	Gly	Val	Val	50	55	60	
Val	Thr	Leu	Thr	Pro	Glu	Asn	Asn	Leu	Arg	Thr	Leu	Ser	Ser	Gln	65	70	75	
His	Gly	Leu	Gly	Gly	Cys	Asp	Gln	Ser	Val	Met	Asp	Leu	Ile	Lys	80	85	90	
Arg	Asn	Ser	Gly	Trp	Val	Phe	Glu	Asn	Pro	Ser	Ile	Gly	Val	Leu	95	100	105	
Glu	Leu	Trp	Val	Leu	Ala	Thr	Asn	Phe	Arg	Asp	Tyr	Ala	Ile	Ile	110	115	120	
Phe	Thr	Gln	Leu	Glu	Phe	Gly	Asp	Glu	Pro	Phe	Asn	Thr	Val	Glu	125	130	135	
Leu	Tyr	Ser	Leu	Thr	Glu	Thr	Ala	Ser	Gln	Glu	Ala	Met	Gly	Leu	140	145	150	
Phe	Thr	Lys	Trp	Ser	Arg	Ser	Leu	Gly	Phe	Leu	Ser	Gln	155	160				

<210> 159

<211> 1665

<212> DNA

<213> Homo sapiens

<400> 159

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gtaaactgct gacgatgcag agttccgtga cgggtgcagga aggcctgtgt 150
gtccatgtgc cctgctcctt ctctacccc tcgcatggct ggatttaccc 200
tggcccagta gttcatggct actggttccg ggaagggggc aatacagacc 250
aggatgctcc agtggccaca aacaaccag ctcgggcagt gtgggaggag 300
actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350
cctgagcatc agagatgcca gaagaagtga tgcggggaga tacttctttc 400
gtatggagaa aggaagtata aaatggaatt ataaacatca ccggctctct 450
gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500
cctggagtcc ggctgcccc agaatctgac ctgctctgtg ccctgggcct 550
gtgagcaggg gacaccccct atgatctcct ggatagggac ctccgtgtcc 600
cccctggacc cctccaccac ccgctcctcg gtgctcacc tcatcccaca 650
gccccaggac catggcacca gcctcacctg tcaggtgacc ttccctgggg 700
ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctacccgcct 750
cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800
cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgcgcc 850
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gggtgctggag ctgccttggg tgcacctgag ggatgcagct gaattcacct 1000
gcagagctca gaaccctctc ggctctcagc aggtctacct gaacgtctcc 1050
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acgggcatag aggatgcaaa cgctgtcagg ggttcagcct ctcaggggcc 1250
cctgactgaa ccttgggcag aagacagtcc ccagaccag cctccccag 1300

cttctgccccg ctcctcagtg ggggaaggag agctccagta tgcattccctc 1350
 agcttccaga tggatgaagcc ttgggactcg cggggacagg aggcactga 1400
 caccgagtac tcggagatca agatccacag atgagaaaact gcagagactc 1450
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 tgattcttgt agaattaaca gccctcaacg tgatgagcta tgataacact 1550
 atgaattatg tgcagagtga aaagcacaca ggctttagag tcaaagtatc 1600
 tcaaacctga atccacactg tgccctccct tttatttttt taactaaaag 1650
 acagacaaat tccta 1665

<210> 160

<211> 463

<212> PRT

<213> Homo sapiens

<400> 160

Met	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Trp	Gly	Arg	Glu	Arg	Ala	1	5	10	15
Glu	Gly	Gln	Thr	Ser	Lys	Leu	Leu	Thr	Met	Gln	Ser	Ser	Val	Thr	20	25	30	
Val	Gln	Glu	Gly	Leu	Cys	Val	His	Val	Pro	Cys	Ser	Phe	Ser	Tyr	35	40	45	
Pro	Ser	His	Gly	Trp	Ile	Tyr	Pro	Gly	Pro	Val	Val	His	Gly	Tyr	50	55	60	
Trp	Phe	Arg	Glu	Gly	Ala	Asn	Thr	Asp	Gln	Asp	Ala	Pro	Val	Ala	65	70	75	
Thr	Asn	Asn	Pro	Ala	Arg	Ala	Val	Trp	Glu	Glu	Thr	Arg	Asp	Arg	80	85	90	
Phe	His	Leu	Leu	Gly	Asp	Pro	His	Thr	Lys	Asn	Cys	Thr	Leu	Ser	95	100	105	
Ile	Arg	Asp	Ala	Arg	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Phe	Phe	Arg	110	115	120	
Met	Glu	Lys	Gly	Ser	Ile	Lys	Trp	Asn	Tyr	Lys	His	His	Arg	Leu	125	130	135	
Ser	Val	Asn	Val	Thr	Ala	Leu	Thr	His	Arg	Pro	Asn	Ile	Leu	Ile	140	145	150	
Pro	Gly	Thr	Leu	Glu	Ser	Gly	Cys	Pro	Gln	Asn	Leu	Thr	Cys	Ser	155	160	165	
Val	Pro	Trp	Ala	Cys	Glu	Gln	Gly	Thr	Pro	Pro	Met	Ile	Ser	Trp	170	175	180	

Ile Gly Thr Ser	Val Ser Pro Leu Asp	Pro Ser Thr Thr Arg Ser
	185	190 195
Ser Val Leu Thr	Leu Ile Pro Gln Pro	Gln Asp His Gly Thr Ser
	200	205 210
Leu Thr Cys Gln	Val Thr Phe Pro Gly	Ala Ser Val Thr Thr Asn
	215	220 225
Lys Thr Val His	Leu Asn Val Ser Tyr	Pro Pro Gln Asn Leu Thr
	230	235 240
Met Thr Val Phe	Gln Gly Asp Gly Thr	Val Ser Thr Val Leu Gly
	245	250 255
Asn Gly Ser Ser	Leu Ser Leu Pro Glu	Gly Gln Ser Leu Arg Leu
	260	265 270
Val Cys Ala Val	Asp Ala Val Asp Ser	Asn Pro Pro Ala Arg Leu
	275	280 285
Ser Leu Ser Trp	Arg Gly Leu Thr Leu	Cys Pro Ser Gln Pro Ser
	290	295 300
Asn Pro Gly Val	Leu Glu Leu Pro Trp	Val His Leu Arg Asp Ala
	305	310 315
Ala Glu Phe Thr	Cys Arg Ala Gln Asn	Pro Leu Gly Ser Gln Gln
	320	325 330
Val Tyr Leu Asn	Val Ser Leu Gln Ser	Lys Ala Thr Ser Gly Val
	335	340 345
Thr Gln Gly Val	Val Gly Gly Ala Gly	Ala Thr Ala Leu Val Phe
	350	355 360
Leu Ser Phe Cys	Val Ile Phe Val Val	Val Arg Ser Cys Arg Lys
	365	370 375
Lys Ser Ala Arg	Pro Ala Ala Gly Val	Gly Asp Thr Gly Ile Glu
	380	385 390
Asp Ala Asn Ala	Val Arg Gly Ser Ala	Ser Gln Gly Pro Leu Thr
	395	400 405
Glu Pro Trp Ala	Glu Asp Ser Pro Pro	Asp Gln Pro Pro Pro Ala
	410	415 420
Ser Ala Arg Ser	Ser Val Gly Glu Gly	Glu Leu Gln Tyr Ala Ser
	425	430 435
Leu Ser Phe Gln	Met Val Lys Pro Trp	Asp Ser Arg Gly Gln Glu
	440	445 450
Ala Thr Asp Thr	Glu Tyr Ser Glu Ile	Lys Ile His Arg
	455	460

<210> 161
<211> 739
<212> DNA
<213> Homo sapiens

<400> 161
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accctgttcc tgggtgtcac gctcggcctg gccgctgccc tgctcttcac 100
cctggaggag gaggatatca cagggacctg gtacgtgaag gccatggtgg 150
tcgataagga ctttccggag gacaggaggc ccaggaaggt gtccccagtg 200
aaggtgacag ccctgggcgg tgggaagttg gaagccacgt tcaccttcat 250
gagggaggat cggtgcatcc agaagaaaat cctgatgcgg aagacggagg 300
agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350
gagctgcccc ggagggacca ctacatcttt tactgcaaag accagcacca 400
tgggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450
accgggaggc cctggaagaa ttttaagaaat tgggtgcagcg caagggactc 500
tcggaggagg acattttcac gcccctgcag acgggaagct gcgttcccga 550
aactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600
acacagagcc cggaccacct ggacctacc tccagccatg acccttcctt 650
gtccccaccc acctgactcc aaataaagtc cttttccccc aaaaaaaaaa 700
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162
<211> 170
<212> PRT
<213> Homo sapiens

<400> 162
Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala
1 5 10 15
Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr
20 25 30
Val Lys Ala Met Val Val Asp Lys Asp Phe Pro Glu Asp Arg Arg
35 40 45
Pro Arg Lys Val Ser Pro Val Lys Val Thr Ala Leu Gly Gly Gly
50 55 60
Lys Leu Glu Ala Thr Phe Thr Phe Met Arg Glu Asp Arg Cys Ile
65 70 75

Gln Lys Lys Ile Leu Met Arg Lys Thr Glu Glu Pro Gly Lys Tyr
80 85 90

Ser Ala Tyr Gly Gly Arg Lys Leu Met Tyr Leu Gln Glu Leu Pro
95 100 105

Arg Arg Asp His Tyr Ile Phe Tyr Cys Lys Asp Gln His His Gly
110 115 120

Gly Leu Leu His Met Gly Lys Leu Val Gly Arg Asn Ser Asp Thr
125 130 135

Asn Arg Glu Ala Leu Glu Glu Phe Lys Lys Leu Val Gln Arg Lys
140 145 150

Gly Leu Ser Glu Glu Asp Ile Phe Thr Pro Leu Gln Thr Gly Ser
155 160 165

Cys Val Pro Glu His
170

<210> 163

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 163

ggagatgaag accctgttcc tg 22

<210> 164

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 164

ggagatgaag accctgttcc tgggtg 26

<210> 165

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 165

gtcctccgga aagtccttat c 21

<210> 166

<211> 25

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 166
gcctagtgtt cggaacgca gcttc 25

<210> 167
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 167
caggacctg gtacgtgaag gccatggtgg tcgataagga cttccggag 50

<210> 168
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 168
ctgtccttca ccctggagga ggaggatata acaggacct ggtac 45

<210> 169
<211> 1204
<212> DNA
<213> Homo sapiens

<400> 169
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cagagggtctc acagcagcca aggaacctgg ggcccgtctc tccccctcc 100
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggtt 150
gtagggggag agaccaggat catcaagggg ttcgagtgc agcctcactc 200
ccagccctgg caggcagccc tggtcgagaa gacgcggcta ctctgtggg 250
cgacgtcat cgccccaga tggctcctga cagcagcca ctgcctcaag 300
ccccgtaca tagttcacct ggggcagcac aacctcaga aggaggagg 350
ctgtgagcag acccggacag cactgagtc cttccccac ccgggttca 400
acaacagcct cccaacaaa gaccaccgca atgacatcat gctggtgaag 450
atggcatcgc cagtctccat cacctgggct gtgcgacccc tcacctctc 500

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ctcacgctgt gtcactgctg gcaccagctg cctcatttcc ggctggggca 550
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cacagacacc atgggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700
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<210> 170

<211> 250

<212> PRT

<213> Homo sapiens

<400> 170

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Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu
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Val Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro
             20             25             30

His Ser Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu
             35             40             45

Leu Cys Gly Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala
             50             55             60

Ala His Cys Leu Lys Pro Arg Tyr Ile Val His Leu Gly Gln His
             65             70             75

Asn Leu Gln Lys Glu Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr
             80             85             90

Glu Ser Phe Pro His Pro Gly Phe Asn Asn Ser Leu Pro Asn Lys
             95             100            105

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Asp	His	Arg	Asn	Asp	Ile	Met	Leu	Val	Lys	Met	Ala	Ser	Pro	Val	
				110					115					120	
Ser	Ile	Thr	Trp	Ala	Val	Arg	Pro	Leu	Thr	Leu	Ser	Ser	Arg	Cys	
				125					130					135	
Val	Thr	Ala	Gly	Thr	Ser	Cys	Leu	Ile	Ser	Gly	Trp	Gly	Ser	Thr	
				140					145					150	
Ser	Ser	Pro	Gln	Leu	Arg	Leu	Pro	His	Thr	Leu	Arg	Cys	Ala	Asn	
				155					160					165	
Ile	Thr	Ile	Ile	Glu	His	Gln	Lys	Cys	Glu	Asn	Ala	Tyr	Pro	Gly	
				170					175					180	
Asn	Ile	Thr	Asp	Thr	Met	Val	Cys	Ala	Ser	Val	Gln	Glu	Gly	Gly	
				185					190					195	
Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn	
				200					205					210	
Gln	Ser	Leu	Gln	Gly	Ile	Ile	Ser	Trp	Gly	Gln	Asp	Pro	Cys	Ala	
				215					220					225	
Ile	Thr	Arg	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Cys	Lys	Tyr	Val	
				230					235					240	
Asp	Trp	Ile	Gln	Glu	Thr	Met	Lys	Asn	Asn						
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<210> 171
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 171
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<210> 172
 <211> 24
 <212> DNA
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<220>
 <223> Synthetic oligonucleotide probe

<400> 172
 ctccaggcca tgaggattct gcag 24

<210> 173
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<220>
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aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50

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gagagaccag gatcatcaag gggttcgagt gcaagcctca ctc 43

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<212> DNA
<213> Homo sapiens

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<211> 222
<212> PRT
<213> Homo sapiens

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Ser	Thr	Glu	Glu	Val	Lys	Ile	Glu	Val	Leu	His	Arg	Pro	Glu	Asn	35	40	45
Cys	Ser	Lys	Thr	Ser	Lys	Lys	Gly	Asp	Leu	Leu	Asn	Ala	His	Tyr	50	55	60
Asp	Gly	Tyr	Leu	Ala	Lys	Asp	Gly	Ser	Lys	Phe	Tyr	Cys	Ser	Arg	65	70	75
Thr	Gln	Asn	Glu	Gly	His	Pro	Lys	Trp	Phe	Val	Leu	Gly	Val	Gly	80	85	90
Gln	Val	Ile	Lys	Gly	Leu	Asp	Ile	Ala	Met	Thr	Asp	Met	Cys	Pro	95	100	105
Gly	Glu	Lys	Arg	Lys	Val	Val	Ile	Pro	Pro	Ser	Phe	Ala	Tyr	Gly	110	115	120
Lys	Glu	Gly	Tyr	Ala	Glu	Gly	Lys	Ile	Pro	Pro	Asp	Ala	Thr	Leu	125	130	135
Ile	Phe	Glu	Ile	Glu	Leu	Tyr	Ala	Val	Thr	Lys	Gly	Pro	Arg	Ser	140	145	150
Ile	Glu	Thr	Phe	Lys	Gln	Ile	Asp	Met	Asp	Asn	Asp	Arg	Gln	Leu	155	160	165
Ser	Lys	Ala	Glu	Ile	Asn	Leu	Tyr	Leu	Gln	Arg	Glu	Phe	Glu	Lys	170	175	180
Asp	Glu	Lys	Pro	Arg	Asp	Lys	Ser	Tyr	Gln	Asp	Ala	Val	Leu	Glu	185	190	195
Asp	Ile	Phe	Lys	Lys	Asn	Asp	His	Asp	Gly	Asp	Gly	Phe	Ile	Ser	200	205	210
Pro	Lys	Glu	Tyr	Asn	Val	Tyr	Gln	His	Asp	Glu	Leu				215	220	

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<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 181

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<210> 182

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
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<400> 182
gacatggaca atgacagg 18

<210> 183
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<400> 183
cctttcagga tgtaggag 18

<210> 184
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<400> 184
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<223> Synthetic oligonucleotide probe

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<210> 187
<211> 52
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 187

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cc 52

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<211> 573

<212> DNA

<213> Homo sapiens

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<211> 74

<212> PRT

<213> Homo sapiens

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Leu	Phe	Gly	Ala	Val	Thr	Gln	Lys	Thr	Lys	Thr	Ser	Cys	Ala	Lys
				20					25					30

Cys	Pro	Pro	Asn	Ala	Ser	Cys	Val	Asn	Asn	Thr	His	Cys	Thr	Cys
				35						40				45

Asn	His	Gly	Tyr	Thr	Ser	Gly	Ser	Gly	Gln	Lys	Leu	Phe	Thr	Phe
				50					55					60

Pro	Leu	Glu	Thr	Cys	Asn	Ala	Arg	His	Gly	Gly	Ser	Arg	Leu
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<210> 191
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 191
cgttacatgt ctccaagggg aatg 24

<210> 192
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 192
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<210> 193
<211> 1091
<212> DNA
<213> Homo sapiens

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<210> 194

<211> 248

<212> PRT

<213> Homo sapiens

<400> 194

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Asn	Ser	Gln	Pro	Trp	Gln	Val	Gly	Leu	Phe	Glu	Gly	Thr	Ser	Leu	35	40	45	
Arg	Cys	Gly	Gly	Val	Leu	Ile	Asp	His	Arg	Trp	Val	Leu	Thr	Ala	50	55	60	
Ala	His	Cys	Ser	Gly	Ser	Arg	Tyr	Trp	Val	Arg	Leu	Gly	Glu	His	65	70	75	
Ser	Leu	Ser	Gln	Leu	Asp	Trp	Thr	Glu	Gln	Ile	Arg	His	Ser	Gly	80	85	90	
Phe	Ser	Val	Thr	His	Pro	Gly	Tyr	Leu	Gly	Ala	Ser	Thr	Ser	His	95	100	105	
Glu	His	Asp	Leu	Arg	Leu	Leu	Arg	Leu	Arg	Leu	Pro	Val	Arg	Val	110	115	120	

Thr	Ser	Ser	Val	Gln	Pro	Leu	Pro	Leu	Pro	Asn	Asp	Cys	Ala	Thr	
				125					130					135	
Ala	Gly	Thr	Glu	Cys	His	Val	Ser	Gly	Trp	Gly	Ile	Thr	Asn	His	
				140					145					150	
Pro	Arg	Asn	Pro	Phe	Pro	Asp	Leu	Leu	Gln	Cys	Leu	Asn	Leu	Ser	
				155					160					165	
Ile	Val	Ser	His	Ala	Thr	Cys	His	Gly	Val	Tyr	Pro	Gly	Arg	Ile	
				170					175					180	
Thr	Ser	Asn	Met	Val	Cys	Ala	Gly	Gly	Val	Pro	Gly	Gln	Asp	Ala	
				185					190					195	
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gly	Gly	Val	Leu	
				200					205					210	
Gln	Gly	Leu	Val	Ser	Trp	Gly	Ser	Val	Gly	Pro	Cys	Gly	Gln	Asp	
				215					220					225	
Gly	Ile	Pro	Gly	Val	Tyr	Thr	Tyr	Ile	Cys	Lys	Tyr	Val	Asp	Trp	
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				245											

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<210> 196

<211> 150

<212> PRT

<213> Homo sapiens

<400> 196

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				20					25					30
Arg	Glu	Phe	Leu	Cys	Asp	Gln	Lys	Tyr	Ser	Asp	Glu	Glu	Asn	Leu
				35					40					45
Pro	Glu	Lys	Leu	Thr	Ala	Phe	Lys	Glu	Lys	Tyr	Met	Glu	Phe	Asp
				50					55					60
Leu	Asn	Asn	Glu	Gly	Glu	Ile	Asp	Leu	Met	Ser	Leu	Lys	Arg	Met
				65					70					75

Met	Glu	Lys	Leu	Gly	Val	Pro	Lys	Thr	His	Leu	Glu	Met	Lys	Lys
				80					85					90
Met	Ile	Ser	Glu	Val	Thr	Gly	Gly	Val	Ser	Asp	Thr	Ile	Ser	Tyr
				95					100					105
Arg	Asp	Phe	Val	Asn	Met	Met	Leu	Gly	Lys	Arg	Ser	Ala	Val	Leu
				110					115					120
Lys	Leu	Val	Met	Met	Phe	Glu	Gly	Lys	Ala	Asn	Glu	Ser	Ser	Pro
				125					130					135
Lys	Pro	Val	Gly	Pro	Pro	Pro	Glu	Arg	Asp	Ile	Ala	Ser	Leu	Pro
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<211> 4842

<212> DNA

<213> Homo sapiens

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tccaaccaca gtgtacagtg tggagacagt gaatgatggg cagtttcaca 3800
 gtgtggagct ggtgacgcta aaccagaccc tgaacctagt agtggacaaa 3850
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 gactctgcca atgcctgctc agccttcaag tgtcaccatg ggcagtgcc 4350
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 gcccatcatg gaatgtcgtg ggggctgtgg gcccagtgcc tgccagccca 4550
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<210> 198

<211> 1523

<212> PRT

<213> Homo sapiens

<400> 198

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Ala Val Ala Cys Pro Thr Lys Cys Thr Cys Ser Ala Ala Ser Val

35										40					45				
Asp	Cys	His	Gly	Leu	Gly	Leu	Arg	Ala	Val	Pro	Arg	Gly	Ile	Pro					
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Arg	Asn	Ala	Glu	Arg	Leu	Asp	Leu	Asp	Arg	Asn	Asn	Ile	Thr	Arg					
65										70					75				
Ile	Thr	Lys	Met	Asp	Phe	Ala	Gly	Leu	Lys	Asn	Leu	Arg	Val	Leu					
80										85					90				
His	Leu	Glu	Asp	Asn	Gln	Val	Ser	Val	Ile	Glu	Arg	Gly	Ala	Phe					
95										100					105				
Gln	Asp	Leu	Lys	Gln	Leu	Glu	Arg	Leu	Arg	Leu	Asn	Lys	Asn	Lys					
110										115					120				
Leu	Gln	Val	Leu	Pro	Glu	Leu	Leu	Phe	Gln	Ser	Thr	Pro	Lys	Leu					
125										130					135				
Thr	Arg	Leu	Asp	Leu	Ser	Glu	Asn	Gln	Ile	Gln	Gly	Ile	Pro	Arg					
140										145					150				
Lys	Ala	Phe	Arg	Gly	Ile	Thr	Asp	Val	Lys	Asn	Leu	Gln	Leu	Asp					
155										160					165				
Asn	Asn	His	Ile	Ser	Cys	Ile	Glu	Asp	Gly	Ala	Phe	Arg	Ala	Leu					
170										175					180				
Arg	Asp	Leu	Glu	Ile	Leu	Thr	Leu	Asn	Asn	Asn	Asn	Ile	Ser	Arg					
185										190					195				
Ile	Leu	Val	Thr	Ser	Phe	Asn	His	Met	Pro	Lys	Ile	Arg	Thr	Leu					
200										205					210				
Arg	Leu	His	Ser	Asn	His	Leu	Tyr	Cys	Asp	Cys	His	Leu	Ala	Trp					
215										220					225				
Leu	Ser	Asp	Trp	Leu	Arg	Gln	Arg	Arg	Thr	Val	Gly	Gln	Phe	Thr					
230										235					240				
Leu	Cys	Met	Ala	Pro	Val	His	Leu	Arg	Gly	Phe	Asn	Val	Ala	Asp					
245										250					255				
Val	Gln	Lys	Lys	Glu	Tyr	Val	Cys	Pro	Ala	Pro	His	Ser	Glu	Pro					
260										265					270				
Pro	Ser	Cys	Asn	Ala	Asn	Ser	Ile	Ser	Cys	Pro	Ser	Pro	Cys	Thr					
275										280					285				
Cys	Ser	Asn	Asn	Ile	Val	Asp	Cys	Arg	Gly	Lys	Gly	Leu	Met	Glu					
290										295					300				
Ile	Pro	Ala	Asn	Leu	Pro	Glu	Gly	Ile	Val	Glu	Ile	Arg	Leu	Glu					
305										310					315				
Gln	Asn	Ser	Ile	Lys	Ala	Ile	Pro	Ala	Gly	Ala	Phe	Thr	Gln	Tyr					

320					325					330				
Lys	Lys	Leu	Lys	Arg	Ile	Asp	Ile	Ser	Lys	Asn	Gln	Ile	Ser	Asp
				335					340					345
Ile	Ala	Pro	Asp	Ala	Phe	Gln	Gly	Leu	Lys	Ser	Leu	Thr	Ser	Leu
				350					355					360
Val	Leu	Tyr	Gly	Asn	Lys	Ile	Thr	Glu	Ile	Ala	Lys	Gly	Leu	Phe
				365					370					375
Asp	Gly	Leu	Val	Ser	Leu	Gln	Leu	Leu	Leu	Leu	Asn	Ala	Asn	Lys
				380					385					390
Ile	Asn	Cys	Leu	Arg	Val	Asn	Thr	Phe	Gln	Asp	Leu	Gln	Asn	Leu
				395					400					405
Asn	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Lys	Leu	Gln	Thr	Ile	Ser	Lys
				410					415					420
Gly	Leu	Phe	Ala	Pro	Leu	Gln	Ser	Ile	Gln	Thr	Leu	His	Leu	Ala
				425					430					435
Gln	Asn	Pro	Phe	Val	Cys	Asp	Cys	His	Leu	Lys	Trp	Leu	Ala	Asp
				440					445					450
Tyr	Leu	Gln	Asp	Asn	Pro	Ile	Glu	Thr	Ser	Gly	Ala	Arg	Cys	Ser
				455					460					465
Ser	Pro	Arg	Arg	Leu	Ala	Asn	Lys	Arg	Ile	Ser	Gln	Ile	Lys	Ser
				470					475					480
Lys	Lys	Phe	Arg	Cys	Ser	Gly	Ser	Glu	Asp	Tyr	Arg	Ser	Arg	Phe
				485					490					495
Ser	Ser	Glu	Cys	Phe	Met	Asp	Leu	Val	Cys	Pro	Glu	Lys	Cys	Arg
				500					505					510
Cys	Glu	Gly	Thr	Ile	Val	Asp	Cys	Ser	Asn	Gln	Lys	Leu	Val	Arg
				515					520					525
Ile	Pro	Ser	His	Leu	Pro	Glu	Tyr	Val	Thr	Asp	Leu	Arg	Leu	Asn
				530					535					540
Asp	Asn	Glu	Val	Ser	Val	Leu	Glu	Ala	Thr	Gly	Ile	Phe	Lys	Lys
				545					550					555
Leu	Pro	Asn	Leu	Arg	Lys	Ile	Asn	Leu	Ser	Asn	Asn	Lys	Ile	Lys
				560					565					570
Glu	Val	Arg	Glu	Gly	Ala	Phe	Asp	Gly	Ala	Ala	Ser	Val	Gln	Glu
				575					580					585
Leu	Met	Leu	Thr	Gly	Asn	Gln	Leu	Glu	Thr	Val	His	Gly	Arg	Val
				590					595					600
Phe	Arg	Gly	Leu	Ser	Gly	Leu	Lys	Thr	Leu	Met	Leu	Arg	Ser	Asn

605					610					615				
Leu	Ile	Ser	Cys	Val	Ser	Asn	Asp	Thr	Phe	Ala	Gly	Leu	Ser	Ser
				620					625					630
Val	Arg	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Arg	Ile	Thr	Thr	Ile	Thr
				635					640					645
Pro	Gly	Ala	Phe	Thr	Thr	Leu	Val	Ser	Leu	Ser	Thr	Ile	Asn	Leu
				650					655					660
Leu	Ser	Asn	Pro	Phe	Asn	Cys	Asn	Cys	His	Leu	Ala	Trp	Leu	Gly
				665					670					675
Lys	Trp	Leu	Arg	Lys	Arg	Arg	Ile	Val	Ser	Gly	Asn	Pro	Arg	Cys
				680					685					690
Gln	Lys	Pro	Phe	Phe	Leu	Lys	Glu	Ile	Pro	Ile	Gln	Asp	Val	Ala
				695					700					705
Ile	Gln	Asp	Phe	Thr	Cys	Asp	Gly	Asn	Glu	Glu	Ser	Ser	Cys	Gln
				710					715					720
Leu	Ser	Pro	Arg	Cys	Pro	Glu	Gln	Cys	Thr	Cys	Met	Glu	Thr	Val
				725					730					735
Val	Arg	Cys	Ser	Asn	Lys	Gly	Leu	Arg	Ala	Leu	Pro	Arg	Gly	Met
				740					745					750
Pro	Lys	Asp	Val	Thr	Glu	Leu	Tyr	Leu	Glu	Gly	Asn	His	Leu	Thr
				755					760					765
Ala	Val	Pro	Arg	Glu	Leu	Ser	Ala	Leu	Arg	His	Leu	Thr	Leu	Ile
				770					775					780
Asp	Leu	Ser	Asn	Asn	Ser	Ile	Ser	Met	Leu	Thr	Asn	Tyr	Thr	Phe
				785					790					795
Ser	Asn	Met	Ser	His	Leu	Ser	Thr	Leu	Ile	Leu	Ser	Tyr	Asn	Arg
				800					805					810
Leu	Arg	Cys	Ile	Pro	Val	His	Ala	Phe	Asn	Gly	Leu	Arg	Ser	Leu
				815					820					825
Arg	Val	Leu	Thr	Leu	His	Gly	Asn	Asp	Ile	Ser	Ser	Val	Pro	Glu
				830					835					840
Gly	Ser	Phe	Asn	Asp	Leu	Thr	Ser	Leu	Ser	His	Leu	Ala	Leu	Gly
				845					850					855
Thr	Asn	Pro	Leu	His	Cys	Asp	Cys	Ser	Leu	Arg	Trp	Leu	Ser	Glu
				860					865					870
Trp	Val	Lys	Ala	Gly	Tyr	Lys	Glu	Pro	Gly	Ile	Ala	Arg	Cys	Ser
				875					880					885
Ser	Pro	Glu	Pro	Met	Ala	Asp	Arg	Leu	Leu	Leu	Thr	Thr	Pro	Thr

890	895	900
His Arg Phe Gln Cys Lys Gly Pro Val Asp Ile Asn Ile Val Ala		
905	910	915
Lys Cys Asn Ala Cys Leu Ser Ser Pro Cys Lys Asn Asn Gly Thr		
920	925	930
Cys Thr Gln Asp Pro Val Glu Leu Tyr Arg Cys Ala Cys Pro Tyr		
935	940	945
Ser Tyr Lys Gly Lys Asp Cys Thr Val Pro Ile Asn Thr Cys Ile		
950	955	960
Gln Asn Pro Cys Gln His Gly Gly Thr Cys His Leu Ser Asp Ser		
965	970	975
His Lys Asp Gly Phe Ser Cys Ser Cys Pro Leu Gly Phe Glu Gly		
980	985	990
Gln Arg Cys Glu Ile Asn Pro Asp Asp Cys Glu Asp Asn Asp Cys		
995	1000	1005
Glu Asn Asn Ala Thr Cys Val Asp Gly Ile Asn Asn Tyr Val Cys		
1010	1015	1020
Ile Cys Pro Pro Asn Tyr Thr Gly Glu Leu Cys Asp Glu Val Ile		
1025	1030	1035
Asp His Cys Val Pro Glu Leu Asn Leu Cys Gln His Glu Ala Lys		
1040	1045	1050
Cys Ile Pro Leu Asp Lys Gly Phe Ser Cys Glu Cys Val Pro Gly		
1055	1060	1065
Tyr Ser Gly Lys Leu Cys Glu Thr Asp Asn Asp Asp Cys Val Ala		
1070	1075	1080
His Lys Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly		
1085	1090	1095
Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Glu		
1100	1105	1110
His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln		
1115	1120	1125
Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Glu		
1130	1135	1140
Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Glu		
1145	1150	1155
Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Glu		
1160	1165	1170
Leu Ala Ser Ala Lys Val Arg Pro Gln Ala Asn Ile Ser Leu Gln		

1175	1180	1185
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp		
1190	1195	1200
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu		
1205	1210	1215
Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val		
1220	1225	1230
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr		
1235	1240	1245
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys		
1250	1255	1260
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser		
1265	1270	1275
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala		
1280	1285	1290
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys		
1295	1300	1305
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala		
1310	1315	1320
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys		
1325	1330	1335
Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser		
1340	1345	1350
Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp		
1355	1360	1365
Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly		
1370	1375	1380
Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu		
1385	1390	1395
Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn		
1400	1405	1410
Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser		
1415	1420	1425
Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly		
1430	1435	1440
Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg		
1445	1450	1455
Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala		

1460	1465	1470
Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln		
1475	1480	1485
Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln		
1490	1495	1500
Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu		
1505	1510	1515
Glu Cys Gly Cys Leu Ala Cys Ser		
1520		

<210> 199

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 199

atggagattc ctgccaaactt gccg 24

<210> 200

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 200

ttgttggcat tgaggaggag cagc 24

<210> 201

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 201

gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 50

<210> 202

<211> 753

<212> DNA

<213> Homo sapiens

<400> 202

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gtttcttccg cagactcaac tgagaagtca gcctctgggg caggcaccag 100

gaatctgcct tttcagttct gtctccggca ggctttgagg atgaaggctg 150
 cgggcattct gaccctcatt ggctgcctgg tcacaggcgc cgagtccaaa 200
 atctacactc gttgcaaact ggcaaaaata ttctcgaggg ctggcctgga 250
 caattactgg ggcttcagcc ttggaaactg gatctgcatg gcatattatg 300
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 gactatggca tcttcagat caacagcttc gcgtggtgca gacgcggaaa 400
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 caaggaatga actattggca aggctggaag aaacattgtg agggcagaga 550
 cctgtccgag tggaaaaaag gctgtgaggt ttcctaaact ggaactggac 600
 ccaggatgct ttgcagcaac gccctaggat ttgcagtga tgtccaaatg 650
 cctgtgtcat cttgtcccg ttcctcccaa tttccttct caaacttgga 700
 gagggaaaat taagctatac ttttaagaaa ataaatattt ccatttaa 750
 gtc 753

<210> 203

<211> 148

<212> PRT

<213> Homo sapiens

<400> 203

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Gly	Ala	Glu	Ser	Lys	Ile	Tyr	Thr	Arg	Cys	Lys	Leu	Ala	Lys	Ile
				20					25					30
Phe	Ser	Arg	Ala	Gly	Leu	Asp	Asn	Tyr	Trp	Gly	Phe	Ser	Leu	Gly
				35					40					45
Asn	Trp	Ile	Cys	Met	Ala	Tyr	Tyr	Glu	Ser	Gly	Tyr	Asn	Thr	Thr
				50					55					60
Ala	Pro	Thr	Val	Leu	Asp	Asp	Gly	Ser	Ile	Asp	Tyr	Gly	Ile	Phe
				65					70					75
Gln	Ile	Asn	Ser	Phe	Ala	Trp	Cys	Arg	Arg	Gly	Lys	Leu	Lys	Glu
				80					85					90
Asn	Asn	His	Cys	His	Val	Ala	Cys	Ser	Ala	Leu	Ile	Thr	Asp	Asp
				95					100					105
Leu	Thr	Asp	Ala	Ile	Ile	Cys	Ala	Arg	Lys	Ile	Val	Lys	Glu	Thr
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Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly
125 130 135

Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser
140 145

<210> 204

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 204

gcaggctttg aggatgaagg ctgc 24

<210> 205

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 205

ctcattggct gcctggtcac aggc 24

<210> 206

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 206

ccagtcggac aggtctctcc cctc 24

<210> 207

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 207

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<210> 208

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 208

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<210> 209

<211> 1648

<212> DNA

<213> Homo sapiens

<400> 209

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ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200
gcggaagaag atcctatttt actgtcactt cccagatctg cttctcacca 250
agagagattc ttttcttaaa cgactataca gggccccaat tgactggata 300
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cacagctgct gtttttaagg aaacattcaa gtccctgtct cacatagacc 400
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acattatcag gaattgaaga aaatgggtcca acagtccgac cttggccagt 700
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 tgctcttctg tctataaatt ttgaatgata ctgtgcctta attgggttttc 1400
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 ataatgagag cagggctatt gtagttccca gattcaatcc accgaagtgt 1500
 tcactgtcat ctgttaggga atttttgttt gtccctgtctt tgcctggatc 1550
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 actgagatat aataaaaggt gtttatcata aaaaaaaaaa aaaaaaaaa 1648

<210> 210

<211> 323

<212> PRT

<213> Homo sapiens

<400> 210

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Glu	Lys	Phe	Lys	Leu	Phe	Thr	Leu	Val	Ser	Ala	Cys	Ile	Pro	Val	20	25	30	
Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	Ile	Leu	Phe	Tyr	Cys	His	35	40	45	
Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	Ser	Phe	Leu	Lys	Arg	50	55	60	
Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	Tyr	Thr	Thr	Gly	65	70	75	
Met	Ala	Asp	Cys	Ile	Leu	Val	Asn	Ser	Gln	Phe	Thr	Ala	Ala	Val	80	85	90	
Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	Asp	Val	95	100	105	
Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	Pro	110	115	120	
Glu	Lys	Leu	Asp	Asp	Leu	Val	Pro	Lys	Gly	Lys	Lys	Phe	Leu	Leu	125	130	135	
Leu	Ser	Ile	Asn	Arg	Tyr	Glu	Arg	Lys	Lys	Asn	Leu	Thr	Leu	Ala	140	145	150	
Leu	Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp				

	155	160	165
Trp Glu Arg Val	His Leu Ile Val Ala	Gly Gly Tyr Asp Glu Arg	
	170	175	180
Val Leu Glu Asn Val	Glu His Tyr Gln	Glu Leu Lys Lys Met Val	
	185	190	195
Gln Gln Ser Asp	Leu Gly Gln Tyr Val	Thr Phe Leu Arg Ser Phe	
	200	205	210
Ser Asp Lys Gln	Lys Ile Ser Leu Leu	His Ser Cys Thr Cys Val	
	215	220	225
Leu Tyr Thr Pro	Ser Asn Glu His Phe	Gly Ile Val Pro Leu Glu	
	230	235	240
Ala Met Tyr Met	Gln Cys Pro Val Ile	Ala Val Asn Ser Gly Gly	
	245	250	255
Pro Leu Glu Ser	Ile Asp His Ser Val	Thr Gly Phe Leu Cys Glu	
	260	265	270
Pro Asp Pro Val	His Phe Ser Glu Ala	Ile Glu Lys Phe Ile Arg	
	275	280	285
Glu Pro Ser Leu	Lys Ala Thr Met Gly	Leu Ala Gly Arg Ala Arg	
	290	295	300
Val Lys Glu Lys	Phe Ser Pro Glu Ala	Phe Thr Glu Gln Leu Tyr	
	305	310	315
Arg Tyr Val Thr	Lys Leu Leu Val		
	320		

<210> 211
 <211> 1554
 <212> DNA
 <213> Homo sapiens

<400> 211
 gactacgccg atccgagacg tggctccctg ggcggcagaa ccatgttgga 50
 cttcgcgata ttgcgcgtta ccttcttgct ggcgttggtg ggagccgtgc 100
 totacctcta tccggttcc agacaagctg caggaattcc agggattact 150
 ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtggaag 200
 tttgcatgag ttcttggtta atttgcata gagatatggg cctgtggtct 250
 ccttctgggtt tggcaggcgc ctcttggtta gtttgggcac tgttgatgta 300
 ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaacat 350
 gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtgaaa 400

accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450
 agtaactttg ccctcctcct aaagctttca gaagaattat tagataaatg 500
 gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550
 gttttgctat gaagtctgtt acacagatgg taatgggtag tacatttgaa 600
 gatgatcagg aagtcattcg cttccagaag aatcatggca cagtttggtc 650
 tgagattgga aaaggctttc tagatgggtc acttgataaa aacatgactc 700
 ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750
 aacatcataa aagaacgaaa aggaaggaac ttcagtcaac atattttcat 800
 tgactcctta gtacaaggga accttaatga ccaacagatc ctagaagaca 850
 gtatgatatt ttctctggcc agttgcataa taaactgcaa attgtgtacc 900
 tgggcaatct gttttttaac cacctctgaa gaagttcaaa aaaaattata 950
 tgaagagata aaccaagttt ttggaaatgg tcctgttact ccagagaaaa 1000
 ttgagcagct cagatattgt cagcatgtgc tttgtgaaac tgttcgaact 1050
 gccaaactga ctccagtttc tgcccagctt caagatattg aaggaaaaat 1100
 tgaccgattt attattccta gagagaccct cgtcctttat gcccttggtg 1150
 tgg tacttca ggatcctaact acttggccat ctccacacaa gtttgatcca 1200
 gatcggtttg atgatgaatt agtaatgaaa actttttcct cacttggtt 1250
 ctcaggcaca caggagtgtc cagagttgag gtttgcatat atggtgacca 1300
 cagtacttct tagtgtattg gtgaagagac tgcacctact ttctgtggag 1350
 ggacaggtta ttgaaacaaa gtatgaactg gtaacatcat caagggaaga 1400
 agcttggtatc actgtctcaa agagatatta aaattttata catttaaaat 1450
 cattgttaaa ttgattgagg aaaacaacca tttaaaaaaa atctatgttg 1500
 aatcctttta taaaccagta tcactttgta atataaacac ctatttgtac 1550
 ttaa 1554

<210> 212

<211> 462

<212> PRT

<213> Homo sapiens

<400> 212

Met	Leu	Asp	Phe	Ala	Ile	Phe	Ala	Val	Thr	Phe	Leu	Leu	Ala	Leu
1					5				10					15

Val Gly Ala Val	Leu Tyr Leu Tyr Pro	Ala Ser Arg Gln Ala Ala	
	20	25	30
Gly Ile Pro Gly	Ile Thr Pro Thr Glu	Glu Lys Asp Gly Asn Leu	
	35	40	45
Pro Asp Ile Val	Asn Ser Gly Ser Leu	His Glu Phe Leu Val Asn	
	50	55	60
Leu His Glu Arg	Tyr Gly Pro Val Val	Ser Phe Trp Phe Gly Arg	
	65	70	75
Arg Leu Val Val	Ser Leu Gly Thr Val	Asp Val Leu Lys Gln His	
	80	85	90
Ile Asn Pro Asn	Lys Thr Ser Asp Pro	Phe Glu Thr Met Leu Lys	
	95	100	105
Ser Leu Leu Arg	Tyr Gln Ser Gly Gly	Gly Ser Val Ser Glu Asn	
	110	115	120
His Met Arg Lys	Lys Leu Tyr Glu Asn	Gly Val Thr Asp Ser Leu	
	125	130	135
Lys Ser Asn Phe	Ala Leu Leu Leu Lys	Leu Ser Glu Glu Leu Leu	
	140	145	150
Asp Lys Trp Leu	Ser Tyr Pro Glu Thr	Gln His Val Pro Leu Ser	
	155	160	165
Gln His Met Leu	Gly Phe Ala Met Lys	Ser Val Thr Gln Met Val	
	170	175	180
Met Gly Ser Thr	Phe Glu Asp Asp Gln	Glu Val Ile Arg Phe Gln	
	185	190	195
Lys Asn His Gly	Thr Val Trp Ser Glu	Ile Gly Lys Gly Phe Leu	
	200	205	210
Asp Gly Ser Leu	Asp Lys Asn Met Thr	Arg Lys Lys Gln Tyr Glu	
	215	220	225
Asp Ala Leu Met	Gln Leu Glu Ser Val	Leu Arg Asn Ile Ile Lys	
	230	235	240
Glu Arg Lys Gly	Arg Asn Phe Ser Gln	His Ile Phe Ile Asp Ser	
	245	250	255
Leu Val Gln Gly	Asn Leu Asn Asp Gln	Gln Ile Leu Glu Asp Ser	
	260	265	270
Met Ile Phe Ser	Leu Ala Ser Cys Ile	Ile Thr Ala Lys Leu Cys	
	275	280	285
Thr Trp Ala Ile	Cys Phe Leu Thr Thr	Ser Glu Glu Val Gln Lys	
	290	295	300

Lys	Leu	Tyr	Glu	Glu	Ile	Asn	Gln	Val	Phe	Gly	Asn	Gly	Pro	Val	
				305						310				315	
Thr	Pro	Glu	Lys	Ile	Glu	Gln	Leu	Arg	Tyr	Cys	Gln	His	Val	Leu	
				320						325				330	
Cys	Glu	Thr	Val	Arg	Thr	Ala	Lys	Leu	Thr	Pro	Val	Ser	Ala	Gln	
				335						340				345	
Leu	Gln	Asp	Ile	Glu	Gly	Lys	Ile	Asp	Arg	Phe	Ile	Ile	Pro	Arg	
				350						355				360	
Glu	Thr	Leu	Val	Leu	Tyr	Ala	Leu	Gly	Val	Val	Leu	Gln	Asp	Pro	
				365						370				375	
Asn	Thr	Trp	Pro	Ser	Pro	His	Lys	Phe	Asp	Pro	Asp	Arg	Phe	Asp	
				380						385				390	
Asp	Glu	Leu	Val	Met	Lys	Thr	Phe	Ser	Ser	Leu	Gly	Phe	Ser	Gly	
				395						400				405	
Thr	Gln	Glu	Cys	Pro	Glu	Leu	Arg	Phe	Ala	Tyr	Met	Val	Thr	Thr	
				410						415				420	
Val	Leu	Leu	Ser	Val	Leu	Val	Lys	Arg	Leu	His	Leu	Leu	Ser	Val	
				425						430				435	
Glu	Gly	Gln	Val	Ile	Glu	Thr	Lys	Tyr	Glu	Leu	Val	Thr	Ser	Ser	
				440						445				450	
Arg	Glu	Glu	Ala	Trp	Ile	Thr	Val	Ser	Lys	Arg	Tyr				
				455						460					

<210> 213
 <211> 759
 <212> DNA
 <213> Homo sapiens

<400> 213
 ctagatttgt cggcttgccg ggagacttca ggagtcgctg tctctgaact 50
 tccagcctca gagaccgccg cccttgctcc cgagggccat gggccgggtc 100
 tcagggcttg tgccctctcg ctctctgacg ctctggcgc atctggtggt 150
 cgatcatcacc ttattctggt cccgggacag caacatacag gcctgcctgc 200
 ctctcacgtt caccctcgag gaggatgaca agcaggacat tcagctggtg 250
 gccgcgtct ctgtaccct gggcctcttt gcagtggagc tggccgggtt 300
 cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350
 gggctcactg tagtgcaccc gtggccctgt ccttcttcat attcgagcgt 400
 tgggagtgca ctacgtattg gtacattttt gtcttctgca gtgcccttcc 450

agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500
aacccttctg attaccttca tgacgggaac ctaaggacga agcctacagg 550
ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcgggtt 600
ttcccctcgg aaactgcttc tgctggagga tatgtgttgg aataattacg 650
tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaata 700
tgttttgtag taacattaag acttatatac agttttaggg gacaattaaa 750
aaaaaaaa 759

<210> 214
<211> 140
<212> PRT
<213> Homo sapiens

<400> 214
Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu
1 5 10 15
Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp
20 25 30
Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu
35 40 45
Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr
50 55 60
Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val
65 70 75
Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His
80 85 90
Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp
95 100 105
Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu
110 115 120
Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu
125 130 135
Lys Lys Lys Pro Phe
140

<210> 215
<211> 697
<212> DNA
<213> Homo sapiens

<400> 215
tcccggaacc tgccgcctg ccactatgtc ccgcccgtct atgctgcttg 50

cctgggctct cccagcctc ctctgactcg gagcggctca ggagacagaa 100
gacccggcct gctgcagccc catagtgcc cggaacgagt ggaaggccct 150
ggcatcagag tgcgcccagc acctgagcct gcccttacgc tatgtggtgg 200
tatcgcacac ggcgggcagc agctgcaaca ccccgccctc gtgccagcag 250
caggcccgga atgtgcagca ctaccacatg aagacactgg gctggtgcga 300
cgtgggctac aacttcctga ttggagaaga cgggctcgta tacgagggcc 350
gtggctggaa cttcacgggt gccactcag gtcacttatg gaaccccatg 400
tccattggca tcagcttcat gggcaactac atggatcggg tgcccacacc 450
ccaggccatc cgggcagccc agggctctact ggctgcgggt gtggctcagg 500
gagccctgag gtccaactat gtgctcaaag gacaccggga tgtgcagcgt 550
aactctctc caggcaacca gctctaccac ctcatccaga attggccaca 600
ctaccgctcc ccctgaggcc ctgctgatcc gcacccatt cctcccctcc 650
catggccaaa aacccactg tctccttctc caataaagat gtagctc 697

<210> 216

<211> 196

<212> PRT

<213> Homo sapiens

<400> 216

Met	Ser	Arg	Arg	Ser	Met	Leu	Leu	Ala	Trp	Ala	Leu	Pro	Ser	Leu
1				5					10					15
Leu	Arg	Leu	Gly	Ala	Ala	Gln	Glu	Thr	Glu	Asp	Pro	Ala	Cys	Cys
			20						25					30
Ser	Pro	Ile	Val	Pro	Arg	Asn	Glu	Trp	Lys	Ala	Leu	Ala	Ser	Glu
			35						40					45
Cys	Ala	Gln	His	Leu	Ser	Leu	Pro	Leu	Arg	Tyr	Val	Val	Val	Ser
			50						55					60
His	Thr	Ala	Gly	Ser	Ser	Cys	Asn	Thr	Pro	Ala	Ser	Cys	Gln	Gln
			65						70					75
Gln	Ala	Arg	Asn	Val	Gln	His	Tyr	His	Met	Lys	Thr	Leu	Gly	Trp
			80						85					90
Cys	Asp	Val	Gly	Tyr	Asn	Phe	Leu	Ile	Gly	Glu	Asp	Gly	Leu	Val
			95						100					105
Tyr	Glu	Gly	Arg	Gly	Trp	Asn	Phe	Thr	Gly	Ala	His	Ser	Gly	His
			110						115					120

Leu	Trp	Asn	Pro	Met	Ser	Ile	Gly	Ile	Ser	Phe	Met	Gly	Asn	Tyr
				125					130					135
Met	Asp	Arg	Val	Pro	Thr	Pro	Gln	Ala	Ile	Arg	Ala	Ala	Gln	Gly
				140					145					150
Leu	Leu	Ala	Cys	Gly	Val	Ala	Gln	Gly	Ala	Leu	Arg	Ser	Asn	Tyr
				155					160					165
Val	Leu	Lys	Gly	His	Arg	Asp	Val	Gln	Arg	Thr	Leu	Ser	Pro	Gly
				170					175					180
Asn	Gln	Leu	Tyr	His	Leu	Ile	Gln	Asn	Trp	Pro	His	Tyr	Arg	Ser
				185					190					195

Pro

<210> 217
 <211> 1871
 <212> DNA
 <213> Homo sapiens

<400> 217
 ctgggacccc gaaaagagaa ggggagagcg aggggacgag agcggaggag 50
 gaagatgcaa ctgactcgct gctgcttcgt gttcctggtg cagggtagcc 100
 tctatctggt catctgtggc caggatgatg gtctctcccg ctcagaggac 150
 cctgagcgtg atgaccacga gggccagccc cgccccggg tgccctcgaa 200
 gcggggccac atctcaccta agtcccgccc catggccaat tccactctcc 250
 tagggctgct ggccccgcct ggggaggctt ggggcattct tgggcagccc 300
 cccaaccgcc cgaaccacag cccccaccc tcagccaagg tgaagaaaat 350
 ctttggtggt ggcgacttct actccaacat caagacggtg gccctgaacc 400
 tgctcgtcac agggaagatt gtggaccatg gcaatgggac cttcagcgtc 450
 cacttccaac acaatgccac aggccaggga aacatctcca tcagcctcgt 500
 gccccccagt aaagctgtag agttccacca ggaacagcag atcttcatcg 550
 aagccaaggc ctccaaaatc ttcaactgcc ggatggagtg ggagaaggta 600
 gaacggggcc gccggacctc gctttgcacc cacgaccag ccaagatctg 650
 ctcccgagac cacgctcaga gctcagccac ctggagctgc tcccagccct 700
 tcaaagtcgt ctgtgtctac atcgcttctt acagcacgga ctatcggctg 750
 gtccagaagg tgtgccaga ttacaactac catagtata cccctacta 800
 cccatctggg tgaccggggg caggccacag aggccaggcc agggctggaa 850

ggacaggcct gcccatgcag gagaccatct ggacaccggg caggaaggg 900
 gttgggcctc aggcaggag ggggtggag acgaggagat gccaaagtgg 950
 gccagggccca agtctcaagt ggcagagaaa ggggtcccaag tgctgggtccc 1000
 aacctgaagc tgtggagtga ctagatcaca ggagcactgg aggaggagtg 1050
 ggctctctgt gcagcctcac agggctttgc cacggagcca cagagagatg 1100
 ctgggtcccc gaggcctgtg ggcaggccga tcagtgtggc cccagatcaa 1150
 gtcattggag gaagctaagc ccttggttct tgccatcctg aggaaagata 1200
 gcaacaggga gggggagatt tcatcagtgt ggacagcctg tcaacttagg 1250
 atggatggct gagagggctt cctaggagcc agtcagcagg gtgggggtgg 1300
 gccagaggag ctctccagcc ctgcctagtg ggcgcctga gcccttgtc 1350
 gtgtgctgag catggcatga ggctgaagtg gcaaccctgg ggtctttgat 1400
 gtcttgacag attgaccatc tgtctccagc caggccaccc ctttccaaaa 1450
 ttccctcttc tgccagtact cccctgtac caccattgc tgatggcaca 1500
 cccatcctta agctaagaca ggacgattgt ggtcctcca cactaaggcc 1550
 acagcccata cgcgtgctgt gtgtccctct tccaccccaa cccctgctgg 1600
 ctctcttggg agcatccatg tcccgagag gggtcctca acagtcagcc 1650
 tcacctgtca gaccggggtt ctccggatc tggatggcgc cgcctctca 1700
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 aaccgctgat tgctgacttt tgtgtgaaga atcgtgttct tggagcagga 1850
 aataaagctt gcccggggc a 1871

<210> 218

<211> 252

<212> PRT

<213> Homo sapiens

<400> 218

Met	Gln	Leu	Thr	Arg	Cys	Cys	Phe	Val	Phe	Leu	Val	Gln	Gly	Ser
1				5					10					15
Leu	Tyr	Leu	Val	Ile	Cys	Gly	Gln	Asp	Asp	Gly	Pro	Pro	Gly	Ser
				20					25					30
Glu	Asp	Pro	Glu	Arg	Asp	Asp	His	Glu	Gly	Gln	Pro	Arg	Pro	Arg
				35					40					45

Val	Pro	Arg	Lys	Arg	Gly	His	Ile	Ser	Pro	Lys	Ser	Arg	Pro	Met
				50					55					60
Ala	Asn	Ser	Thr	Leu	Leu	Gly	Leu	Leu	Ala	Pro	Pro	Gly	Glu	Ala
				65					70					75
Trp	Gly	Ile	Leu	Gly	Gln	Pro	Pro	Asn	Arg	Pro	Asn	His	Ser	Pro
				80					85					90
Pro	Pro	Ser	Ala	Lys	Val	Lys	Lys	Ile	Phe	Gly	Trp	Gly	Asp	Phe
				95					100					105
Tyr	Ser	Asn	Ile	Lys	Thr	Val	Ala	Leu	Asn	Leu	Leu	Val	Thr	Gly
				110					115					120
Lys	Ile	Val	Asp	His	Gly	Asn	Gly	Thr	Phe	Ser	Val	His	Phe	Gln
				125					130					135
His	Asn	Ala	Thr	Gly	Gln	Gly	Asn	Ile	Ser	Ile	Ser	Leu	Val	Pro
				140					145					150
Pro	Ser	Lys	Ala	Val	Glu	Phe	His	Gln	Glu	Gln	Gln	Ile	Phe	Ile
				155					160					165
Glu	Ala	Lys	Ala	Ser	Lys	Ile	Phe	Asn	Cys	Arg	Met	Glu	Trp	Glu
				170					175					180
Lys	Val	Glu	Arg	Gly	Arg	Arg	Thr	Ser	Leu	Cys	Thr	His	Asp	Pro
				185					190					195
Ala	Lys	Ile	Cys	Ser	Arg	Asp	His	Ala	Gln	Ser	Ser	Ala	Thr	Trp
				200					205					210
Ser	Cys	Ser	Gln	Pro	Phe	Lys	Val	Val	Cys	Val	Tyr	Ile	Ala	Phe
				215					220					225
Tyr	Ser	Thr	Asp	Tyr	Arg	Leu	Val	Gln	Lys	Val	Cys	Pro	Asp	Tyr
				230					235					240
Asn	Tyr	His	Ser	Asp	Thr	Pro	Tyr	Tyr	Pro	Ser	Gly			
				245					250					

<210> 219
 <211> 2065
 <212> DNA
 <213> Homo sapiens

<400> 219
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 gcaggggccc caggcagggc tgattcttgg gcggaggaga gtagggtaaa 100
 gggttctgca tgagctcctt aaaggacaaa ggtaacagag ccagcgagag 150
 agctcgaggg gagactttga cttcaagcca cagaattggt ggaagtgtgc 200

gcgcccgcgc cgccgtcgtc cctgcagcgc tgtcgacctc gccgctagca 250
tcttcccagag caccggggtc ccggggtagg aggcgacgcg ggcgagcacc 300
agcgccagcc ggctgcggct gccacacgg ctcaccatgg gctccgggcg 350
ccgggcgctg tccgcgggtg cggccgtgct gctggtcctc acgctgccgg 400
ggctgcccgct ctgggcacag aacgacacgg agcccatcgt gctggagggc 450
aagtgtctgg tgggtgtcga ctgcaacccg gccacggact ccaagggctc 500
ctcttcctcc ccgctgggga tatcggtccg ggcgggccaac tccaaggctc 550
ccttctcggc ggtgcggagc accaaccacg agccatccga gatgagcaac 600
aagacgcgca tcatttactt cgatcagatc ctggtgaatg tgggtaattt 650
tttcacattg gagtctgtct ttgtagcacc aagaaaagga atttacagtt 700
tcagttttca cgtgattaaa gtctaccaga gccaaactat ccagggttaac 750
ttgatgttaa atggaaaacc agtaatatct gcctttgcgg gggacaaaaga 800
tgttactcgt gaagctgccg cgaatggtgt cctgctctac ctagataaag 850
aggataaggt ttacctaaaa ctggagaaaag gtaatttggt tggaggctgg 900
cagtattcca cgttttctgg ctttctgggtg ttccccctat aggattcaat 950
ttctccatga tgttcatcca ggtgagggat gaccactcc tgagttattg 1000
gaagatcatt ttttcatcat tggattgatg ttttttattg gtttctcatg 1050
ggtggatatg gattctaagg attctagcct gtctgaacca atacaaaatt 1100
tcacagatta tttgtgtgtg tctgtttcag tatatttgga ttgggactct 1150
aagcagataa tacctatgct taaatgtaac agtcaaaagc tgtctgcaag 1200
acttattctg aatttcattt cctgggatta ctgaattagt tacagatgtg 1250
gaattttatt tgttttagttt taaaagactg gcaaccaggt ctaaggatta 1300
gaaaactcta aagttctgac ttcaatcaac ggttagtgtg atactgcaa 1350
agaactgtat actgtgttaa tatattgatt atatttgttt ttattccttt 1400
ggaattagtt tgtttggttc ttgtaaaaaa cttggatttt ttttttcagt 1450
aactgggtatt atgttttctc ttaaaataag gtaatgaatg gcttgcccac 1500
aaatttacct tgactacgat atcatcgaca tgacttctct caaaaaaaaa 1550
gaatgcttca tagttgtatt ttaattgtat atgtgaaaga gtcataattt 1600
ccaagttata ttttctaaga agaagaatag atcataaatc tgacaaggaa 1650

aaagttgctt acccaaaatc taagtgtca atccctgagc ctcagcaaaa 1700
 cagctcccct ccgagggaaa tcttatactt tattgctcaa ctttaattaa 1750
 aatgattgat aataaccact ttattaaaaa cctaagggtt tttttttttc 1800
 cgtagacatg accactttat taactgggtg tgggatgctg ttgtttctaa 1850
 ttatacctat ttttcaaggc ttctgttgta tttgaagtat catctgggtt 1900
 tgccttaact ctttaaattg tatatattta tctgttttagc taatattaaa 1950
 ttcaaataat ccatatctaa atttagtgca atatcttgct ttttgtatag 2000
 gtcatatgaa ttcataaaat tatttatgtc tgttatagaa taaagattaa 2050
 tatatgttaa aaaaa 2065

<210> 220

<211> 201

<212> PRT

<213> Homo sapiens

<400> 220

Met	Gly	Ser	Gly	Arg	Arg	Ala	Leu	Ser	Ala	Val	Pro	Ala	Val	Leu
1				5				10						15
Leu	Val	Leu	Thr	Leu	Pro	Gly	Leu	Pro	Val	Trp	Ala	Gln	Asn	Asp
				20				25						30
Thr	Glu	Pro	Ile	Val	Leu	Glu	Gly	Lys	Cys	Leu	Val	Val	Cys	Asp
				35				40						45
Ser	Asn	Pro	Ala	Thr	Asp	Ser	Lys	Gly	Ser	Ser	Ser	Ser	Pro	Leu
				50				55						60
Gly	Ile	Ser	Val	Arg	Ala	Ala	Asn	Ser	Lys	Val	Ala	Phe	Ser	Ala
				65				70						75
Val	Arg	Ser	Thr	Asn	His	Glu	Pro	Ser	Glu	Met	Ser	Asn	Lys	Thr
				80				85						90
Arg	Ile	Ile	Tyr	Phe	Asp	Gln	Ile	Leu	Val	Asn	Val	Gly	Asn	Phe
				95				100						105
Phe	Thr	Leu	Glu	Ser	Val	Phe	Val	Ala	Pro	Arg	Lys	Gly	Ile	Tyr
				110				115						120
Ser	Phe	Ser	Phe	His	Val	Ile	Lys	Val	Tyr	Gln	Ser	Gln	Thr	Ile
				125				130						135
Gln	Val	Asn	Leu	Met	Leu	Asn	Gly	Lys	Pro	Val	Ile	Ser	Ala	Phe
				140				145						150
Ala	Gly	Asp	Lys	Asp	Val	Thr	Arg	Glu	Ala	Ala	Thr	Asn	Gly	Val
				155				160						165

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Arg	Ile	Ile	Phe	Leu	Ile	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser
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Asp	Asn	Lys	Asp	Gly	Pro	Thr	Gln	Lys	Tyr	Leu	Leu	Ile	Phe	Gly
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Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Ser	Glu	Gly	Leu	Lys	Ser	Ile	Asn
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Pro Gly Glu Thr Ala Pro Ser Met Arg Leu Leu Ala Tyr Val Ser	110	115	120
Gly Leu Gly Phe Gly Ile Met Ser Gly Val Phe Ser Phe Val Asn	125	130	135
Thr Leu Ser Asp Ser Leu Gly Pro Gly Thr Val Gly Ile His Gly	140	145	150
Asp Ser Pro Gln Phe Phe Leu Tyr Ser Ala Phe Met Thr Leu Val	155	160	165
Ile Ile Leu Leu His Val Phe Trp Gly Ile Val Phe Phe Asp Gly	170	175	180
Cys Glu Lys Lys Lys Trp Gly Ile Leu Leu Ile Val Leu Leu Thr	185	190	195
His Leu Leu Val Ser Ala Gln Thr Phe Ile Ser Ser Tyr Tyr Gly	200	205	210
Ile Asn Leu Ala Ser Ala Phe Ile Ile Leu Val Leu Met Gly Thr	215	220	225
Trp Ala Phe Leu Ala Ala Gly Gly Ser Cys Arg Ser Leu Lys Leu	230	235	240
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Glu	Leu	Val	Asn	Ile	Tyr	Thr	Phe	Asn	His	Thr	Val	Thr	Arg	Asn
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Arg	Thr	Glu	Gly	Val	Arg	Val	Ser	Val	Asn	Val	Leu	Asn	Lys	Gln
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Lys	Gly	Ala	Pro	Leu	Leu	Phe	Val	Val	Arg	Gln	Lys	Glu	Ala	Val
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Val	Ser	Phe	Gln	Val	Pro	Leu	Ile	Leu	Arg	Gly	Met	Phe	Gln	Arg
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Lys	Tyr	Leu	Tyr	Gln	Lys	Val	Glu	Arg	Thr	Leu	Cys	Gln	Pro	Pro
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Thr	Lys	Asn	Glu	Ser	Glu	Ile	Gln	Phe	Phe	Tyr	Val	Asp	Val	Ser

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Thr	Thr	Ala	Ala	Gln	Pro	Gln	Tyr	Phe	Lys	Tyr	Glu	Phe	Pro	Glu
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Gly	Val	Asp	Ser	Val	Ile	Val	Lys	Val	Thr	Ser	Asn	Lys	Ala	Phe
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Pro	Cys	Ser	Val	Ile	Ser	Ile	Gln	Asp	Val	Leu	Cys	Pro	Val	Tyr
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Thr	Lys	Lys	Ala	Ala	Ile	Thr	Val	Gln	Arg	Lys	Asp	Phe	Pro	Ser
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 tgcaacgtgg aggggcagtg catgcgcaag gtgggccgca tgaaggcat 2400
 gccacgaag ctgtcggcag tgggcatcct tgtaggcacc ctggtagcaa 2450
 taggaatctt cctcatcctc attttcaccc actggaccat gtcaaggaag 2500
 aaggaccgg atcaaccagc agacagcgtg cccctgaagg cgactgtctg 2550
 aatggcccag gcagctctag ctgggagctt ggcctctggc tccatctgag 2600
 tcccctggga gagagcccag cacccaagat ccagcagggg acaggacaga 2650
 gtagaagccc ctccatctgc cctgggggtgg aggcaccatc accatcacca 2700
 ggcatgtctg cagagcctgg acaccaactt tatggactgc ccatgggagt 2750
 gctccaaatg tcagggtgtt tgcccaataa taaagcccca gagaactggg 2800
 ctgggcccta tgggaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaag 2848

<210> 229

<211> 807

<212> PRT

<213> Homo sapiens

<400> 229

Met	Val	Pro	Ala	Trp	Leu	Trp	Leu	Leu	Cys	Val	Ser	Val	Pro	Gln
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Ala	Leu	Pro	Lys	Ala	Gln	Pro	Ala	Glu	Leu	Ser	Val	Glu	Val	Pro
				20					25					30
Glu	Asn	Tyr	Gly	Gly	Asn	Phe	Pro	Leu	Tyr	Leu	Thr	Lys	Leu	Pro
				35					40					45
Leu	Pro	Arg	Glu	Gly	Ala	Glu	Gly	Gln	Ile	Val	Leu	Ser	Gly	Asp
				50					55					60
Ser	Gly	Lys	Ala	Thr	Glu	Gly	Pro	Phe	Ala	Met	Asp	Pro	Asp	Ser
				65					70					75
Gly	Phe	Leu	Leu	Val	Thr	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Gln	Ala

80										85					90				
Glu	Tyr	Gln	Leu	Gln	Val	Thr	Leu	Glu	Met	Gln	Asp	Gly	His	Val					
				95					100					105					
Leu	Trp	Gly	Pro	Gln	Pro	Val	Leu	Val	His	Val	Lys	Asp	Glu	Asn					
				110					115					120					
Asp	Gln	Val	Pro	His	Phe	Ser	Gln	Ala	Ile	Tyr	Arg	Ala	Arg	Leu					
				125					130					135					
Ser	Arg	Gly	Thr	Arg	Pro	Gly	Ile	Pro	Phe	Leu	Phe	Leu	Glu	Ala					
				140					145					150					
Ser	Asp	Arg	Asp	Glu	Pro	Gly	Thr	Ala	Asn	Ser	Asp	Leu	Arg	Phe					
				155					160					165					
His	Ile	Leu	Ser	Gln	Ala	Pro	Ala	Gln	Pro	Ser	Pro	Asp	Met	Phe					
				170					175					180					
Gln	Leu	Glu	Pro	Arg	Leu	Gly	Ala	Leu	Ala	Leu	Ser	Pro	Lys	Gly					
				185					190					195					
Ser	Thr	Ser	Leu	Asp	His	Ala	Leu	Glu	Arg	Thr	Tyr	Gln	Leu	Leu					
				200					205					210					
Val	Gln	Val	Lys	Asp	Met	Gly	Asp	Gln	Ala	Ser	Gly	His	Gln	Ala					
				215					220					225					
Thr	Ala	Thr	Val	Glu	Val	Ser	Ile	Ile	Glu	Ser	Thr	Trp	Val	Ser					
				230					235					240					
Leu	Glu	Pro	Ile	His	Leu	Ala	Glu	Asn	Leu	Lys	Val	Leu	Tyr	Pro					
				245					250					255					
His	His	Met	Ala	Gln	Val	His	Trp	Ser	Gly	Gly	Asp	Val	His	Tyr					
				260					265					270					
His	Leu	Glu	Ser	His	Pro	Pro	Gly	Pro	Phe	Glu	Val	Asn	Ala	Glu					
				275					280					285					
Gly	Asn	Leu	Tyr	Val	Thr	Arg	Glu	Leu	Asp	Arg	Glu	Ala	Gln	Ala					
				290					295					300					
Glu	Tyr	Leu	Leu	Gln	Val	Arg	Ala	Gln	Asn	Ser	His	Gly	Glu	Asp					
				305					310					315					
Tyr	Ala	Ala	Pro	Leu	Glu	Leu	His	Val	Leu	Val	Met	Asp	Glu	Asn					
				320					325					330					
Asp	Asn	Val	Pro	Ile	Cys	Pro	Pro	Arg	Asp	Pro	Thr	Val	Ser	Ile					
				335					340					345					
Pro	Glu	Leu	Ser	Pro	Pro	Gly	Thr	Glu	Val	Thr	Arg	Leu	Ser	Ala					
				350					355					360					
Glu	Asp	Ala	Asp	Ala	Pro	Gly	Ser	Pro	Asn	Ser	His	Val	Val	Tyr					

	365	370	375
Gln Leu Leu Ser	Pro Glu Pro Glu Asp	Gly Val Glu Gly Arg	Ala
	380	385	390
Phe Gln Val Asp	Pro Thr Ser Gly Ser	Val Thr Leu Gly Val	Leu
	395	400	405
Pro Leu Arg Ala	Gly Gln Asn Ile Leu	Leu Leu Val Leu Ala	Met
	410	415	420
Asp Leu Ala Gly	Ala Glu Gly Gly Phe	Ser Ser Thr Cys Glu	Val
	425	430	435
Glu Val Ala Val	Thr Asp Ile Asn Asp	His Ala Pro Glu Phe	Ile
	440	445	450
Thr Ser Gln Ile	Gly Pro Ile Ser Leu	Pro Glu Asp Val Glu	Pro
	455	460	465
Gly Thr Leu Val	Ala Met Leu Thr Ala	Ile Asp Ala Asp Leu	Glu
	470	475	480
Pro Ala Phe Arg	Leu Met Asp Phe Ala	Ile Glu Arg Gly Asp	Thr
	485	490	495
Glu Gly Thr Phe	Gly Leu Asp Trp Glu	Pro Asp Ser Gly His	Val
	500	505	510
Arg Leu Arg Leu	Cys Lys Asn Leu Ser	Tyr Glu Ala Ala Pro	Ser
	515	520	525
His Glu Val Val	Val Val Val Gln Ser	Val Ala Lys Leu Val	Gly
	530	535	540
Pro Gly Pro Gly	Pro Gly Ala Thr Ala	Thr Val Thr Val Leu	Val
	545	550	555
Glu Arg Val Met	Pro Pro Pro Lys Leu	Asp Gln Glu Ser Tyr	Glu
	560	565	570
Ala Ser Val Pro	Ile Ser Ala Pro Ala	Gly Ser Phe Leu Leu	Thr
	575	580	585
Ile Gln Pro Ser	Asp Pro Ile Ser Arg	Thr Leu Arg Phe Ser	Leu
	590	595	600
Val Asn Asp Ser	Glu Gly Trp Leu Cys	Ile Glu Lys Phe Ser	Gly
	605	610	615
Glu Val His Thr	Ala Gln Ser Leu Gln	Gly Ala Gln Pro Gly	Asp
	620	625	630
Thr Tyr Thr Val	Leu Val Glu Ala Gln	Asp Thr Ala Leu Thr	Leu
	635	640	645
Ala Pro Val Pro	Ser Gln Tyr Leu Cys	Thr Pro Arg Gln Asp	His

650										655					660				
Gly	Leu	Ile	Val	Ser	Gly	Pro	Ser	Lys	Asp	Pro	Asp	Leu	Ala	Ser					
				665					670					675					
Gly	His	Gly	Pro	Tyr	Ser	Phe	Thr	Leu	Gly	Pro	Asn	Pro	Thr	Val					
				680					685					690					
Gln	Arg	Asp	Trp	Arg	Leu	Gln	Thr	Leu	Asn	Gly	Ser	His	Ala	Tyr					
				695					700					705					
Leu	Thr	Leu	Ala	Leu	His	Trp	Val	Glu	Pro	Arg	Glu	His	Ile	Ile					
				710					715					720					
Pro	Val	Val	Val	Ser	His	Asn	Ala	Gln	Met	Trp	Gln	Leu	Leu	Val					
				725					730					735					
Arg	Val	Ile	Val	Cys	Arg	Cys	Asn	Val	Glu	Gly	Gln	Cys	Met	Arg					
				740					745					750					
Lys	Val	Gly	Arg	Met	Lys	Gly	Met	Pro	Thr	Lys	Leu	Ser	Ala	Val					
				755					760					765					
Gly	Ile	Leu	Val	Gly	Thr	Leu	Val	Ala	Ile	Gly	Ile	Phe	Leu	Ile					
				770					775					780					
Leu	Ile	Phe	Thr	His	Trp	Thr	Met	Ser	Arg	Lys	Lys	Asp	Pro	Asp					
				785					790					795					
Gln	Pro	Ala	Asp	Ser	Val	Pro	Leu	Lys	Ala	Thr	Val								
				800					805										

<210> 230

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 230

cgcccttaccg cgcagcccga agattcacta tgggtgaaaat cgccttcaat 50

<210> 231

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 231

cctgagctgt aaccccactc cagg 24

<210> 232

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 232

agagtctgtc ccagctatct tgt 23

<210> 233

<211> 2786

<212> DNA

<213> Homo sapiens

<400> 233

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atctgtggcc aagaaaaatt ttttggggac caagttttga ggattaatgt 100
cagaaatgga gacgagatca gcaaattgag tcaactagtg aattcaaaca 150
acttgaagct caatttctgg aaatctccct cctccttcaa tcggcctgtg 200
gatgtcctgg tcccatctgt cagtctgcag gcatttaaata ccttcctgag 250
atcccagggc ttagagtacg cagtgcacaat tgaggacctg caggcccttt 300
tagacaatga agatgatgaa atgcaacaca atgaagggca agaacggagc 350
agtaataact tcaactacgg ggcttaccat tccctggaag ctatttacca 400
cgagatggac aacattgccg cagactttcc tgacctggcg aggaggggtga 450
agattggaca ttcgtttgaa aaccggccga tgtatgtact gaagttcagc 500
actgggaaag gcgtgaggcg gccggccggtt tggctgaatg caggcatcca 550
ttcccgagag tggatctccc aggccactgc aatctggacg gcaaggaaga 600
ttgtatctga ttaccagagg gatccagcta tcacctccat cttggagaaa 650
atggatattt tcttgttgcc tgtggccaat cctgatggat atgtgtatac 700
tcaaactcaa aaccgattat ggaggaagac gcggtcccga aatcctggaa 750
gctcctgcat tgggtgctgac ccaaatagaa actggaacgc tagttttgca 800
ggaaagggag ccagcgacaa cccttgctcc gaagtgtacc atggacccca 850
cgccaattcg gaagtggagg tgaaatcagt ggtagatttc atccaaaaac 900
atgggaattt caagggttc atcgacctgc acagctactc gcagctgctg 950
atgtatccat atgggtactc agtcaaaaag gcccagatg ccgaggaact 1000
cgacaagggtg gcgaggcttg cggccaaagc tctggcttct gtgtcgggca 1050
ctgagtacca agtgggtccc acctgcacca ctgtctatcc agctagcggg 1100

agcagcatcg actgggcgta tgacaacggc atcaaatttg cattcacatt 1150
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tcatccccac tgcagaggag acgtggctgg ggctgaagac catcatggag 1250
catgtgcggg acaacctcta ctaggcgatg gctctgctct gtctacattt 1300
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 agctgcctct tgtttcattt cacctcagca cgtaccatct gtccttttgt 2650
 tgttgttgtt ttgtttttgt ttttttgctt ttaccaaaca tgtctgtaaa 2700
 tcttaacctc ctgcctagga tttgtacagc atctggtgtg tgcttataag 2750
 ccaataaata ttcaatgtga aaaaaaaaaa aaaaaa 2786

<210> 234

<211> 421

<212> PRT

<213> Homo sapiens

<400> 234

Met	Arg	Trp	Ile	Leu	Phe	Ile	Gly	Ala	Leu	Ile	Gly	Ser	Ser	Ile	1	5	10	15
Cys	Gly	Gln	Glu	Lys	Phe	Phe	Gly	Asp	Gln	Val	Leu	Arg	Ile	Asn	20	25	30	
Val	Arg	Asn	Gly	Asp	Glu	Ile	Ser	Lys	Leu	Ser	Gln	Leu	Val	Asn	35	40	45	
Ser	Asn	Asn	Leu	Lys	Leu	Asn	Phe	Trp	Lys	Ser	Pro	Ser	Ser	Phe	50	55	60	
Asn	Arg	Pro	Val	Asp	Val	Leu	Val	Pro	Ser	Val	Ser	Leu	Gln	Ala	65	70	75	
Phe	Lys	Ser	Phe	Leu	Arg	Ser	Gln	Gly	Leu	Glu	Tyr	Ala	Val	Thr	80	85	90	
Ile	Glu	Asp	Leu	Gln	Ala	Leu	Leu	Asp	Asn	Glu	Asp	Asp	Glu	Met	95	100	105	
Gln	His	Asn	Glu	Gly	Gln	Glu	Arg	Ser	Ser	Asn	Asn	Phe	Asn	Tyr	110	115	120	
Gly	Ala	Tyr	His	Ser	Leu	Glu	Ala	Ile	Tyr	His	Glu	Met	Asp	Asn	125	130	135	
Ile	Ala	Ala	Asp	Phe	Pro	Asp	Leu	Ala	Arg	Arg	Val	Lys	Ile	Gly	140	145	150	
His	Ser	Phe	Glu	Asn	Arg	Pro	Met	Tyr	Val	Leu	Lys	Phe	Ser	Thr	155	160	165	
Gly	Lys	Gly	Val	Arg	Arg	Pro	Ala	Val	Trp	Leu	Asn	Ala	Gly	Ile	170	175	180	
His	Ser	Arg	Glu	Trp	Ile	Ser	Gln	Ala	Thr	Ala	Ile	Trp	Thr	Ala	185	190	195	

Arg	Lys	Ile	Val	Ser	Asp	Tyr	Gln	Arg	Asp	Pro	Ala	Ile	Thr	Ser	
				200					205					210	
Ile	Leu	Glu	Lys	Met	Asp	Ile	Phe	Leu	Leu	Pro	Val	Ala	Asn	Pro	
				215					220					225	
Asp	Gly	Tyr	Val	Tyr	Thr	Gln	Thr	Gln	Asn	Arg	Leu	Trp	Arg	Lys	
				230					235					240	
Thr	Arg	Ser	Arg	Asn	Pro	Gly	Ser	Ser	Cys	Ile	Gly	Ala	Asp	Pro	
				245					250					255	
Asn	Arg	Asn	Trp	Asn	Ala	Ser	Phe	Ala	Gly	Lys	Gly	Ala	Ser	Asp	
				260					265					270	
Asn	Pro	Cys	Ser	Glu	Val	Tyr	His	Gly	Pro	His	Ala	Asn	Ser	Glu	
				275					280					285	
Val	Glu	Val	Lys	Ser	Val	Val	Asp	Phe	Ile	Gln	Lys	His	Gly	Asn	
				290					295					300	
Phe	Lys	Gly	Phe	Ile	Asp	Leu	His	Ser	Tyr	Ser	Gln	Leu	Leu	Met	
				305					310					315	
Tyr	Pro	Tyr	Gly	Tyr	Ser	Val	Lys	Lys	Ala	Pro	Asp	Ala	Glu	Glu	
				320					325					330	
Leu	Asp	Lys	Val	Ala	Arg	Leu	Ala	Ala	Lys	Ala	Leu	Ala	Ser	Val	
				335					340					345	
Ser	Gly	Thr	Glu	Tyr	Gln	Val	Gly	Pro	Thr	Cys	Thr	Thr	Val	Tyr	
				350					355					360	
Pro	Ala	Ser	Gly	Ser	Ser	Ile	Asp	Trp	Ala	Tyr	Asp	Asn	Gly	Ile	
				365					370					375	
Lys	Phe	Ala	Phe	Thr	Phe	Glu	Leu	Arg	Asp	Thr	Gly	Thr	Tyr	Gly	
				380					385					390	
Phe	Leu	Leu	Pro	Ala	Asn	Gln	Ile	Ile	Pro	Thr	Ala	Glu	Glu	Thr	
				395					400					405	
Trp	Leu	Gly	Leu	Lys	Thr	Ile	Met	Glu	His	Val	Arg	Asp	Asn	Leu	
				410					415					420	

Tyr

<210> 235

<211> 1743

<212> DNA

<213> Homo sapiens

<400> 235

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tgttccaaaa tggcatctta cctttatgga gtactctttg ctgttggcct 100

ctgtgctcca atctactgtg tgtccccggc caatgcccc agtgcatacc 150
cccgcccttc ctccacaaag agcaccctg cctcacaggt gtattccctc 200
aacaccgact ttgccttccg cctataccgc aggctgggtt tggagacccc 250
gagtcagaac atcttcttct cccctgtgag tgtctccact tccctggcca 300
tgctctccct tggggccac tcagtcacca agaccagat tctccagggc 350
ctgggcttca acctcacaca cacaccagag tctgccatcc accagggctt 400
ccagcacctg gttcaactcac tgactgttcc cagcaaagac ctgacctga 450
agatgggaag tgccctcttc gtcaagaagg agctgcagct gcaggcaaat 500
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tttctccaac ccctccattg cccaggcgag gatcaacagc catgtgaaa 600
agaagacca agggaagggt gtagacataa tccaaggcct tgacctctg 650
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gccctttcac cttgaatata caagaaagaa cttccattc ctggtgggcg 750
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gggagatgcc gtggccttct ttgtcctccc tagcaagggc aagatgaggc 900
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ctccagaaaa ggtggataga ggtgttcac cccagatttt ccatttctgc 1000
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 attcaataaa actaaaatat gaattcaaaa aaaaaaaaaa aaaaaaaaaa 1700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1743

<210> 236

<211> 417

<212> PRT

<213> Homo sapiens

<400> 236

Met	Ala	Ser	Tyr	Leu	Tyr	Gly	Val	Leu	Phe	Ala	Val	Gly	Leu	Cys	1	5	10	15
Ala	Pro	Ile	Tyr	Cys	Val	Ser	Pro	Ala	Asn	Ala	Pro	Ser	Ala	Tyr	20	25	30	
Pro	Arg	Pro	Ser	Ser	Thr	Lys	Ser	Thr	Pro	Ala	Ser	Gln	Val	Tyr	35	40	45	
Ser	Leu	Asn	Thr	Asp	Phe	Ala	Phe	Arg	Leu	Tyr	Arg	Arg	Leu	Val	50	55	60	
Leu	Glu	Thr	Pro	Ser	Gln	Asn	Ile	Phe	Phe	Ser	Pro	Val	Ser	Val	65	70	75	
Ser	Thr	Ser	Leu	Ala	Met	Leu	Ser	Leu	Gly	Ala	His	Ser	Val	Thr	80	85	90	
Lys	Thr	Gln	Ile	Leu	Gln	Gly	Leu	Gly	Phe	Asn	Leu	Thr	His	Thr	95	100	105	
Pro	Glu	Ser	Ala	Ile	His	Gln	Gly	Phe	Gln	His	Leu	Val	His	Ser	110	115	120	
Leu	Thr	Val	Pro	Ser	Lys	Asp	Leu	Thr	Leu	Lys	Met	Gly	Ser	Ala	125	130	135	
Leu	Phe	Val	Lys	Lys	Glu	Leu	Gln	Leu	Gln	Ala	Asn	Phe	Leu	Gly	140	145	150	
Asn	Val	Lys	Arg	Leu	Tyr	Glu	Ala	Glu	Val	Phe	Ser	Thr	Asp	Phe	155	160	165	
Ser	Asn	Pro	Ser	Ile	Ala	Gln	Ala	Arg	Ile	Asn	Ser	His	Val	Lys	170	175	180	
Lys	Lys	Thr	Gln	Gly	Lys	Val	Val	Asp	Ile	Ile	Gln	Gly	Leu	Asp	185	190	195	
Leu	Leu	Thr	Ala	Met	Val	Leu	Val	Asn	His	Ile	Phe	Phe	Lys	Ala	200	205	210	

Lys Trp Glu Lys Pro Phe His Leu Glu Tyr Thr Arg Lys Asn Phe	215	220	225
Pro Phe Leu Val Gly Glu Gln Val Thr Val Gln Val Pro Met Met	230	235	240
His Gln Lys Glu Gln Phe Ala Phe Gly Val Asp Thr Glu Leu Asn	245	250	255
Cys Phe Val Leu Gln Met Asp Tyr Lys Gly Asp Ala Val Ala Phe	260	265	270
Phe Val Leu Pro Ser Lys Gly Lys Met Arg Gln Leu Glu Gln Ala	275	280	285
Leu Ser Ala Arg Thr Leu Ile Lys Trp Ser His Ser Leu Gln Lys	290	295	300
Arg Trp Ile Glu Val Phe Ile Pro Arg Phe Ser Ile Ser Ala Ser	305	310	315
Tyr Asn Leu Glu Thr Ile Leu Pro Lys Met Gly Ile Gln Asn Ala	320	325	330
Phe Asp Lys Asn Ala Asp Phe Ser Gly Ile Ala Lys Arg Asp Ser	335	340	345
Leu Gln Val Ser Lys Ala Thr His Lys Ala Val Leu Asp Val Ser	350	355	360
Glu Glu Gly Thr Glu Ala Thr Ala Ala Thr Thr Thr Lys Phe Ile	365	370	375
Val Arg Ser Lys Asp Gly Pro Ser Tyr Phe Thr Val Ser Phe Asn	380	385	390
Arg Thr Phe Leu Met Met Ile Thr Asn Lys Ala Thr Asp Gly Ile	395	400	405
Leu Phe Leu Gly Lys Val Glu Asn Pro Thr Lys Ser	410	415	

<210> 237

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

caaccatgca aggacagggc agg 23

<210> 238

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 238

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<210> 239

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 239

tgactcgggg tctccaaaac cagc 24

<210> 240

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 240

ggtataggcg gaaggcaaag tcgg 24

<210> 241

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 241

ggcatcttac ctttatggag tactctttgc tgttggcctc tgtgctcc 48

<210> 242

<211> 2436

<212> DNA

<213> Homo sapiens

<400> 242

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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2436

<210> 243

<211> 596

<212> PRT

<213> Homo sapiens

<400> 243

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Leu	His	Leu	Glu	Ala	Ala	Thr	Asn	Ser	Asn	Glu	Thr	Ser	Thr	Ser
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Ala	Asn	Thr	Gly	Ser	Ser	Val	Ile	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				35					40					45
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Val	Ser	Thr	Ala
				50					55					60
Thr	Ile	Ser	Gly	Ser	Ser	Val	Thr	Ser	Asn	Gly	Val	Ser	Ile	Val
				65					70					75
Thr	Asn	Ser	Glu	Phe	His	Thr	Thr	Ser	Ser	Gly	Ile	Ser	Thr	Ala
				80					85					90
Thr	Asn	Ser	Glu	Phe	Ser	Thr	Ala	Ser	Ser	Gly	Ile	Ser	Ile	Ala
				95					100					105

Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
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Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Ser	Thr	Val	
				125					130					135	
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				140					145					150	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	
				155					160					165	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Leu	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				170					175					180	
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				185					190					195	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				200					205					210	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	
				215					220					225	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				230					235					240	
Thr	Asn	Ser	Glu	Ser	Arg	Thr	Thr	Ser	Asn	Gly	Ala	Gly	Thr	Ala	
				245					250					255	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				260					265					270	
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				275					280					285	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				290					295					300	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				305					310					315	
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Gly	Thr	Ala	
				320					325					330	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ile	Ser	Thr	Val	
				335					340					345	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Asn	Thr	Ala	
				350					355					360	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala	
				365					370					375	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				380					385					390	

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Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	410	415	420
Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Glu Ala Ser Thr Ala	425	430	435
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val	440	445	450
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala	455	460	465
Thr Asn Ser Gly Ser Ser Val Thr Ser Ala Gly Ser Gly Thr Ala	470	475	480
Ala Leu Thr Gly Met His Thr Thr Ser His Ser Ala Ser Thr Ala	485	490	495
Val Ser Glu Ala Lys Pro Gly Gly Ser Leu Val Pro Trp Glu Ile	500	505	510
Phe Leu Ile Thr Leu Val Ser Val Val Ala Ala Val Gly Leu Phe	515	520	525
Ala Gly Leu Phe Phe Cys Val Arg Asn Ser Leu Ser Leu Arg Asn	530	535	540
Thr Phe Asn Thr Ala Val Tyr His Pro His Gly Leu Asn His Gly	545	550	555
Leu Gly Pro Gly Pro Gly Gly Asn His Gly Ala Pro His Arg Pro	560	565	570
Arg Trp Ser Pro Asn Trp Phe Trp Arg Arg Pro Val Ser Ser Ile	575	580	585
Ala Met Glu Met Ser Gly Arg Asn Ser Gly Pro	590	595	

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<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 244

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<210> 245

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 245

gtcagagttg gtggctgtgc tagc 24

<210> 246

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

ggagaccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247

<211> 957

<212> DNA

<213> Homo sapiens

<400> 247

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<210> 248

<211> 247

<212> PRT

<213> Homo sapiens

<400> 248

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Leu	Gly	Ala	Leu	Ser	Gly	Trp	Ala	Ala	Ser	Asp	Asp	Pro	Ile	Glu
				20					25					30
Lys	Val	Ile	Glu	Gly	Ile	Asn	Arg	Gly	Leu	Ser	Asn	Ala	Glu	Arg
				35					40					45
Glu	Val	Gly	Lys	Ala	Leu	Asp	Gly	Ile	Asn	Ser	Gly	Ile	Thr	His
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Ala	Gly	Arg	Glu	Val	Glu	Lys	Val	Phe	Asn	Gly	Leu	Ser	Asn	Met
				65					70					75
Gly	Ser	His	Thr	Gly	Lys	Glu	Leu	Asp	Lys	Gly	Val	Gln	Gly	Leu
				80					85					90
Asn	His	Gly	Met	Asp	Lys	Val	Ala	His	Glu	Ile	Asn	His	Gly	Ile
				95					100					105
Gly	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	Leu	Gly	His	Gly	Val	Asn
				110					115					120
Asn	Ala	Ala	Gly	Gln	Ala	Gly	Lys	Glu	Ala	Asp	Lys	Ala	Val	Gln
				125					130					135
Gly	Phe	His	Thr	Gly	Val	His	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys
				140					145					150
Leu	Gly	Gln	Gly	Val	Asn	His	Ala	Ala	Asp	Gln	Ala	Gly	Lys	Glu
				155					160					165
Val	Glu	Lys	Leu	Gly	Gln	Gly	Ala	His	His	Ala	Ala	Gly	Gln	Ala
				170					175					180
Gly	Lys	Glu	Leu	Gln	Asn	Ala	His	Asn	Gly	Val	Asn	Gln	Ala	Ser
				185					190					195
Lys	Glu	Ala	Asn	Gln	Leu	Leu	Asn	Gly	Asn	His	Gln	Ser	Gly	Ser
				200					205					210
Ser	Ser	His	Gln	Gly	Gly	Ala	Thr	Thr	Thr	Pro	Leu	Ala	Ser	Gly

	215	220	225
Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg			
	230	235	240
Ser Val Ala Asn Ile Met Pro			
	245		

<210> 249
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 249
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<210> 250
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 250
 aagcttctct gcttcctttc ctgc 24

<210> 251
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 251
 tgacccatt gagaaggatc ttgaaggat caaccgagg ctg 43

<210> 252
 <211> 3781
 <212> DNA
 <213> Homo sapiens

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<210> 253

<211> 837

<212> PRT

<213> Homo sapiens

<400> 253

Met	Leu	Arg	Thr	Ala	Met	Gly	Leu	Arg	Ser	Trp	Leu	Ala	Ala	Pro
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Trp	Gly	Ala	Leu	Pro	Pro	Arg	Pro	Pro	Leu	Leu	Leu	Leu	Leu	Leu
				20					25					30
Leu	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Pro	Pro	Thr	Trp	Ala	Leu	Ser
				35					40					45
Pro	Arg	Ile	Ser	Leu	Pro	Leu	Gly	Ser	Glu	Glu	Arg	Pro	Phe	Leu
				50					55					60
Arg	Phe	Glu	Ala	Glu	His	Ile	Ser	Asn	Tyr	Thr	Ala	Leu	Leu	Leu
				65					70					75
Ser	Arg	Asp	Gly	Arg	Thr	Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Leu
				80					85					90
Phe	Ala	Leu	Ser	Ser	Asn	Leu	Ser	Phe	Leu	Pro	Gly	Gly	Glu	Tyr
				95					100					105
Gln	Glu	Leu	Leu	Trp	Gly	Ala	Asp	Ala	Glu	Lys	Lys	Gln	Gln	Cys
				110					115					120

Ser Phe Lys Gly	Lys Asp Pro Gln Arg	Asp Cys Gln Asn Tyr Ile
125	130	135
Lys Ile Leu Leu	Pro Leu Ser Gly Ser	His Leu Phe Thr Cys Gly
140	145	150
Thr Ala Ala Phe	Ser Pro Met Cys Thr	Tyr Ile Asn Met Glu Asn
155	160	165
Phe Thr Leu Ala	Arg Asp Glu Lys Gly	Asn Val Leu Leu Glu Asp
170	175	180
Gly Lys Gly Arg	Cys Pro Phe Asp Pro	Asn Phe Lys Ser Thr Ala
185	190	195
Leu Val Val Asp	Gly Glu Leu Tyr Thr	Gly Thr Val Ser Ser Phe
200	205	210
Gln Gly Asn Asp	Pro Ala Ile Ser Arg	Ser Gln Ser Leu Arg Pro
215	220	225
Thr Lys Thr Glu	Ser Ser Leu Asn Trp	Leu Gln Asp Pro Ala Phe
230	235	240
Val Ala Ser Ala	Tyr Ile Pro Glu Ser	Leu Gly Ser Leu Gln Gly
245	250	255
Asp Asp Asp Lys	Ile Tyr Phe Phe Phe	Ser Glu Thr Gly Gln Glu
260	265	270
Phe Glu Phe Phe	Glu Asn Thr Ile Val	Ser Arg Ile Ala Arg Ile
275	280	285
Cys Lys Gly Asp	Glu Gly Gly Glu Arg	Val Leu Gln Gln Arg Trp
290	295	300
Thr Ser Phe Leu	Lys Ala Gln Leu Leu	Cys Ser Arg Pro Asp Asp
305	310	315
Gly Phe Pro Phe	Asn Val Leu Gln Asp	Val Phe Thr Leu Ser Pro
320	325	330
Ser Pro Gln Asp	Trp Arg Asp Thr Leu	Phe Tyr Gly Val Phe Thr
335	340	345
Ser Gln Trp His	Arg Gly Thr Thr Glu	Gly Ser Ala Val Cys Val
350	355	360
Phe Thr Met Lys	Asp Val Gln Arg Val	Phe Ser Gly Leu Tyr Lys
365	370	375
Glu Val Asn Arg	Glu Thr Gln Gln Trp	Tyr Thr Val Thr His Pro
380	385	390
Val Pro Thr Pro	Arg Pro Gly Ala Cys	Ile Thr Asn Ser Ala Arg
395	400	405

Glu Arg Lys Ile Asn Ser Ser Leu Gln Leu Pro Asp Arg Val Leu	410	415	420
Asn Phe Leu Lys Asp His Phe Leu Met Asp Gly Gln Val Arg Ser	425	430	435
Arg Met Leu Leu Leu Gln Pro Gln Ala Arg Tyr Gln Arg Val Ala	440	445	450
Val His Arg Val Pro Gly Leu His His Thr Tyr Asp Val Leu Phe	455	460	465
Leu Gly Thr Gly Asp Gly Arg Leu His Lys Ala Val Ser Val Gly	470	475	480
Pro Arg Val His Ile Ile Glu Glu Leu Gln Ile Phe Ser Ser Gly	485	490	495
Gln Pro Val Gln Asn Leu Leu Leu Asp Thr His Arg Gly Leu Leu	500	505	510
Tyr Ala Ala Ser His Ser Gly Val Val Gln Val Pro Met Ala Asn	515	520	525
Cys Ser Leu Tyr Arg Ser Cys Gly Asp Cys Leu Leu Ala Arg Asp	530	535	540
Pro Tyr Cys Ala Trp Ser Gly Ser Ser Cys Lys His Val Ser Leu	545	550	555
Tyr Gln Pro Gln Leu Ala Thr Arg Pro Trp Ile Gln Asp Ile Glu	560	565	570
Gly Ala Ser Ala Lys Asp Leu Cys Ser Ala Ser Ser Val Val Ser	575	580	585
Pro Ser Phe Val Pro Thr Gly Glu Lys Pro Cys Glu Gln Val Gln	590	595	600
Phe Gln Pro Asn Thr Val Asn Thr Leu Ala Cys Pro Leu Leu Ser	605	610	615
Asn Leu Ala Thr Arg Leu Trp Leu Arg Asn Gly Ala Pro Val Asn	620	625	630
Ala Ser Ala Ser Cys His Val Leu Pro Thr Gly Asp Leu Leu Leu	635	640	645
Val Gly Thr Gln Gln Leu Gly Glu Phe Gln Cys Trp Ser Leu Glu	650	655	660
Glu Gly Phe Gln Gln Leu Val Ala Ser Tyr Cys Pro Glu Val Val	665	670	675
Glu Asp Gly Val Ala Asp Gln Thr Asp Glu Gly Gly Ser Val Pro	680	685	690

Val	Ile	Ile	Ser	Thr	Ser	Arg	Val	Ser	Ala	Pro	Ala	Gly	Gly	Lys	
				695					700					705	
Ala	Ser	Trp	Gly	Ala	Asp	Arg	Ser	Tyr	Trp	Lys	Glu	Phe	Leu	Val	
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Met	Cys	Thr	Leu	Phe	Val	Leu	Ala	Val	Leu	Leu	Pro	Val	Leu	Phe	
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Leu	Leu	Tyr	Arg	His	Arg	Asn	Ser	Met	Lys	Val	Phe	Leu	Lys	Gln	
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Gly	Glu	Cys	Ala	Ser	Val	His	Pro	Lys	Thr	Cys	Pro	Val	Val	Leu	
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Pro	Pro	Glu	Thr	Arg	Pro	Leu	Asn	Gly	Leu	Gly	Pro	Pro	Ser	Thr	
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Pro	Leu	Asp	His	Arg	Gly	Tyr	Gln	Ser	Leu	Ser	Asp	Ser	Pro	Pro	
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Gly	Ala	Arg	Val	Phe	Thr	Glu	Ser	Glu	Lys	Arg	Pro	Leu	Ser	Ile	
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Gln	Asp	Ser	Phe	Val	Glu	Val	Ser	Pro	Val	Cys	Pro	Arg	Pro	Arg	
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<210> 255

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<223> Synthetic oligonucleotide probe

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gagctgcaga tcttctcatc gggacagccc gtgcagaatc tgctc 45

<210> 259

<211> 4563

<212> DNA

<213> Homo sapiens

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<221> unsure

<222> 3635

<223> unknown base

<400> 259

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tgccggcccc gcgtccccgc gcgcgagcgg gaggagccgc cgccacctcg 200

cgcccagacc gccgctagcg cgccgccggc atggtcccct cttaaaggcg 250

caggccgcgg cgccgggggc ggggtgtgcgg aaaaagcgc cgccgcgggg 300

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gcggcgctgc ccgggcccgg cctcgcggcg ctaggcggg ctggcctccg 400

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<211> 802

<212> PRT

<213> Homo sapiens

<400> 260

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Leu	Val	Leu	Gly	Phe	Val	Leu	Ala	Ser	Arg	Leu	Val	Leu	Pro	Arg
				20					25					30
Ala	Ser	Glu	Leu	Lys	Arg	Ala	Gly	Pro	Arg	Arg	Arg	Ala	Ser	Pro
				35					40					45
Glu	Gly	Cys	Arg	Ser	Gly	Gln	Ala	Ala	Ala	Ser	Gln	Ala	Gly	Gly
				50					55					60
Ala	Arg	Gly	Asp	Ala	Arg	Gly	Ala	Gln	Leu	Trp	Pro	Pro	Gly	Ser
				65					70					75
Asp	Pro	Asp	Gly	Gly	Pro	Arg	Asp	Arg	Asn	Phe	Leu	Phe	Val	Gly
				80					85					90
Val	Met	Thr	Ala	Gln	Lys	Tyr	Leu	Gln	Thr	Arg	Ala	Val	Ala	Ala
				95					100					105
Tyr	Arg	Thr	Trp	Ser	Lys	Thr	Ile	Pro	Gly	Lys	Val	Gln	Phe	Phe
				110					115					120
Ser	Ser	Glu	Gly	Ser	Asp	Thr	Ser	Val	Pro	Ile	Pro	Val	Val	Pro
				125					130					135
Leu	Arg	Gly	Val	Asp	Asp	Ser	Tyr	Pro	Pro	Gln	Lys	Lys	Ser	Phe
				140					145					150
Met	Met	Leu	Lys	Tyr	Met	His	Asp	His	Tyr	Leu	Asp	Lys	Tyr	Glu
				155					160					165
Trp	Phe	Met	Arg	Ala	Asp	Asp	Asp	Val	Tyr	Ile	Lys	Gly	Asp	Arg
				170					175					180
Leu	Glu	Asn	Phe	Leu	Arg	Ser	Leu	Asn	Ser	Ser	Glu	Pro	Leu	Phe
				185					190					195
Leu	Gly	Gln	Thr	Gly	Leu	Gly	Thr	Thr	Glu	Glu	Met	Gly	Lys	Leu
				200					205					210
Ala	Leu	Glu	Pro	Gly	Glu	Asn	Phe	Cys	Met	Gly	Gly	Pro	Gly	Val
				215					220					225
Ile	Met	Ser	Arg	Glu	Val	Leu	Arg	Arg	Met	Val	Pro	His	Ile	Gly
				230					235					240
Lys	Cys	Leu	Arg	Glu	Met	Tyr	Thr	Thr	His	Glu	Asp	Val	Glu	Val
				245					250					255
Gly	Arg	Cys	Val	Arg	Arg	Phe	Ala	Gly	Val	Gln	Cys	Val	Trp	Ser
				260					265					270
Tyr	Glu	Met	Arg	Gln	Leu	Phe	Tyr	Glu	Asn	Tyr	Glu	Gln	Asn	Lys

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Lys	Gly	Tyr	Ile	Arg	Asp	Leu	His	Asn	Ser	Lys	Ile	His	Gln	Ala					
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Ile	Thr	Leu	His	Pro	Asn	Lys	Asn	Pro	Pro	Tyr	Gln	Tyr	Arg	Leu					
				305					310					315					
His	Ser	Tyr	Met	Leu	Ser	Arg	Lys	Ile	Ser	Glu	Leu	Arg	His	Arg					
				320					325					330					
Thr	Ile	Gln	Leu	His	Arg	Glu	Ile	Val	Leu	Met	Ser	Lys	Tyr	Ser					
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Asn	Thr	Glu	Ile	His	Lys	Glu	Asp	Leu	Gln	Leu	Gly	Ile	Pro	Pro					
				350					355					360					
Ser	Phe	Met	Arg	Phe	Gln	Pro	Arg	Gln	Arg	Glu	Glu	Ile	Leu	Glu					
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Trp	Glu	Phe	Leu	Thr	Gly	Lys	Tyr	Leu	Tyr	Ser	Ala	Val	Asp	Gly					
				380					385					390					
Gln	Pro	Pro	Arg	Arg	Gly	Met	Asp	Ser	Ala	Gln	Arg	Glu	Ala	Leu					
				395					400					405					
Asp	Asp	Ile	Val	Met	Gln	Val	Met	Glu	Met	Ile	Asn	Ala	Asn	Ala					
				410					415					420					
Lys	Thr	Arg	Gly	Arg	Ile	Ile	Asp	Phe	Lys	Glu	Ile	Gln	Tyr	Gly					
				425					430					435					
Tyr	Arg	Arg	Val	Asn	Pro	Met	Tyr	Gly	Ala	Glu	Tyr	Ile	Leu	Asp					
				440					445					450					
Leu	Leu	Leu	Leu	Tyr	Lys	Lys	His	Lys	Gly	Lys	Lys	Met	Thr	Val					
				455					460					465					
Pro	Val	Arg	Arg	His	Ala	Tyr	Leu	Gln	Gln	Thr	Phe	Ser	Lys	Ile					
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Gln	Phe	Val	Glu	His	Glu	Glu	Leu	Asp	Ala	Gln	Glu	Leu	Ala	Lys					
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Arg	Ile	Asn	Gln	Glu	Ser	Gly	Ser	Leu	Ser	Phe	Leu	Ser	Asn	Ser					
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Leu	Lys	Lys	Leu	Val	Pro	Phe	Gln	Leu	Pro	Gly	Ser	Lys	Ser	Glu					
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His	Lys	Glu	Pro	Lys	Asp	Lys	Lys	Ile	Asn	Ile	Leu	Ile	Pro	Leu					
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Ser	Gly	Arg	Phe	Asp	Met	Phe	Val	Arg	Phe	Met	Gly	Asn	Phe	Glu					
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Lys	Thr	Cys	Leu	Ile	Pro	Asn	Gln	Asn	Val	Lys	Leu	Val	Val	Leu					

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Leu	Phe	Asn	Ser	Asp	Ser	Asn	Pro	Asp	Lys	Ala	Lys	Gln	Val	Glu					
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Leu	Met	Arg	Asp	Tyr	Arg	Ile	Lys	Tyr	Pro	Lys	Ala	Asp	Met	Gln					
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Ile	Leu	Pro	Val	Ser	Gly	Glu	Phe	Ser	Arg	Ala	Leu	Ala	Leu	Glu					
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Val	Gly	Ser	Ser	Gln	Phe	Asn	Asn	Glu	Ser	Leu	Leu	Phe	Phe	Cys					
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Ala	Asn	Thr	Val	Leu	Gly	Gln	Gln	Ile	Tyr	Phe	Pro	Ile	Ile	Phe					
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Ser	Gln	Tyr	Asp	Pro	Lys	Ile	Val	Tyr	Ser	Gly	Lys	Val	Pro	Ser					
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				680					685					690					
Tyr	Gly	Phe	Gly	Ile	Thr	Cys	Ile	Tyr	Lys	Gly	Asp	Leu	Val	Arg					
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Val	Gly	Gly	Phe	Asp	Val	Ser	Ile	Gln	Gly	Trp	Gly	Leu	Glu	Asp					
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Val	Asp	Leu	Phe	Asn	Lys	Val	Val	Gln	Ala	Gly	Leu	Lys	Thr	Phe					
				725					730					735					
Arg	Ser	Gln	Glu	Val	Gly	Val	Val	His	Val	His	His	Pro	Val	Phe					
				740					745					750					
Cys	Asp	Pro	Asn	Leu	Asp	Pro	Lys	Gln	Tyr	Lys	Met	Cys	Leu	Gly					
				755					760					765					
Ser	Lys	Ala	Ser	Thr	Tyr	Gly	Ser	Thr	Gln	Gln	Leu	Ala	Glu	Met					
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Trp	Leu	Glu	Lys	Asn	Asp	Pro	Ser	Tyr	Ser	Lys	Ser	Ser	Asn	Asn					
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<210> 262

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<400> 263

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<210> 264

<211> 1419

<212> DNA

<213> Homo sapiens

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gcttcacacc ggaaatagga aagaaaaaac acacggaaag tacccttcc 500

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<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

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Ser	Val	Pro	Ala	Tyr	Pro	Ser	Ile	Thr	Val	Thr	Pro	Asp	Glu	Glu
				20					25					30
Gln	Asn	Leu	Asn	His	Tyr	Ile	Gln	Val	Leu	Glu	Asn	Leu	Val	Arg
				35					40					45
Ser	Val	Pro	Ser	Gly	Glu	Pro	Gly	Arg	Glu	Lys	Lys	Ser	Asn	Ser
				50					55					60
Pro	Lys	His	Val	Tyr	Ser	Ile	Ala	Ser	Lys	Gly	Ser	Lys	Phe	Lys
				65					70					75
Glu	Leu	Val	Thr	His	Gly	Asp	Ala	Ser	Thr	Glu	Asn	Asp	Val	Leu
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Thr	Asn	Pro	Ile	Ser	Glu	Glu	Thr	Thr	Thr	Phe	Pro	Thr	Gly	Gly	
				95					100					105	
Phe	Thr	Pro	Glu	Ile	Gly	Lys	Lys	Lys	His	Thr	Glu	Ser	Thr	Pro	
				110					115					120	
Phe	Trp	Ser	Ile	Lys	Pro	Asn	Asn	Val	Ser	Ile	Val	Leu	His	Ala	
				125					130					135	
Glu	Glu	Pro	Tyr	Ile	Glu	Asn	Glu	Glu	Pro	Glu	Pro	Glu	Pro	Glu	
				140					145					150	
Pro	Ala	Ala	Lys	Gln	Thr	Glu	Ala	Pro	Arg	Met	Leu	Pro	Val	Val	
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Thr	Glu	Ser	Ser	Thr	Ser	Pro	Tyr	Val	Thr	Ser	Tyr	Lys	Ser	Pro	
				170					175					180	
Val	Thr	Thr	Leu	Asp	Lys	Ser	Thr	Gly	Ile	Glu	Ile	Ser	Thr	Glu	
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Ser	Glu	Asp	Val	Pro	Gln	Leu	Ser	Gly	Glu	Thr	Ala	Ile	Glu	Lys	
				200					205					210	
Pro	Glu	Glu	Phe	Gly	Lys	His	Pro	Glu	Ser	Trp	Asn	Asn	Asp	Asp	
				215					220					225	
Ile	Leu	Lys	Lys	Ile	Leu	Asp	Ile	Asn	Ser	Gln	Val	Gln	Gln	Ala	
				230					235					240	
Leu	Leu	Ser	Asp	Thr	Ser	Asn	Pro	Ala	Tyr	Arg	Glu	Asp	Ile	Glu	
				245					250					255	
Ala	Ser	Lys	Asp	His	Leu	Lys	Arg	Ser	Leu	Ala	Leu	Ala	Ala	Ala	
				260					265					270	
Ala	Glu	His	Lys	Leu	Lys	Thr	Met	Tyr	Lys	Ser	Gln	Leu	Leu	Pro	
				275					280					285	
Val	Gly	Arg	Thr	Ser	Asn	Lys	Ile	Asp	Asp	Ile	Glu	Thr	Val	Ile	
				290					295					300	
Asn	Met	Leu	Cys	Asn	Ser	Arg	Ser	Lys	Leu	Tyr	Glu	Tyr	Leu	Asp	
				305					310					315	
Ile	Lys	Cys	Val	Pro	Pro	Glu	Met	Arg	Glu	Lys	Ala	Ala	Thr	Val	
				320					325					330	
Phe	Asn	Thr	Leu	Lys	Asn	Met	Cys	Arg	Ser	Arg	Arg	Val	Thr	Ala	
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				350											

<210> 266
 <211> 2403
 <212> DNA

<213> Homo sapiens

<400> 266

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<210> 267

<211> 466

<212> PRT

<213> Homo sapiens

<400> 267

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Ser	Gly	Gln	Trp	Gln	Val	Thr	Gly	Pro	Gly	Lys	Phe	Val	Gln	Ala
				20				25					30	

Leu	Val	Gly	Glu	Asp	Ala	Val	Phe	Ser	Cys	Ser	Leu	Phe	Pro	Glu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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Thr Ser Ala Glu	Ala Met Glu Val Arg Phe	Phe Arg Asn Gln Phe	
	50	55	60
His Ala Val Val	His Leu Tyr Arg Asp Gly	Glu Asp Trp Glu Ser	
	65	70	75
Lys Gln Met Pro	Gln Tyr Arg Gly Arg Thr	Glu Phe Val Lys Asp	
	80	85	90
Ser Ile Ala Gly	Gly Arg Val Ser Leu Arg	Leu Lys Asn Ile Thr	
	95	100	105
Pro Ser Asp Ile	Gly Leu Tyr Gly Cys Trp	Phe Ser Ser Gln Ile	
	110	115	120
Tyr Asp Glu Glu	Ala Thr Trp Glu Leu Arg	Val Ala Ala Leu Gly	
	125	130	135
Ser Leu Pro Leu	Ile Ser Ile Val Gly Tyr	Val Asp Gly Gly Ile	
	140	145	150
Gln Leu Leu Cys	Leu Ser Ser Gly Trp Phe	Pro Gln Pro Thr Ala	
	155	160	165
Lys Trp Lys Gly	Pro Gln Gly Gln Asp Leu	Ser Ser Asp Ser Arg	
	170	175	180
Ala Asn Ala Asp	Gly Tyr Ser Leu Tyr Asp	Val Glu Ile Ser Ile	
	185	190	195
Ile Val Gln Glu	Asn Ala Gly Ser Ile Leu	Cys Ser Ile His Leu	
	200	205	210
Ala Glu Gln Ser	His Glu Val Glu Ser Lys	Val Leu Ile Gly Glu	
	215	220	225
Thr Phe Phe Gln	Pro Ser Pro Trp Arg Leu	Ala Ser Ile Leu Leu	
	230	235	240
Gly Leu Leu Cys	Gly Ala Leu Cys Gly Val	Val Met Gly Met Ile	
	245	250	255
Ile Val Phe Phe	Lys Ser Lys Gly Lys Ile	Gln Ala Glu Leu Asp	
	260	265	270
Trp Arg Arg Lys	His Gly Gln Ala Glu Leu	Arg Asp Ala Arg Lys	
	275	280	285
His Ala Val Glu	Val Thr Leu Asp Pro Glu	Thr Ala His Pro Lys	
	290	295	300
Leu Cys Val Ser	Asp Leu Lys Thr Val Thr	His Arg Lys Ala Pro	
	305	310	315
Gln Glu Val Pro	His Ser Glu Lys Arg Phe	Thr Arg Lys Ser Val	

320	325	330
Val Ala Ser Gln Gly Phe Gln Ala Gly Arg His Tyr Trp Glu Val		
335	340	345
Asp Val Gly Gln Asn Val Gly Trp Tyr Val Gly Val Cys Arg Asp		
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Asp Val Asp Arg Gly Lys Asn Asn Val Thr Leu Ser Pro Asn Asn		
365	370	375
Gly Tyr Trp Val Leu Arg Leu Thr Thr Glu His Leu Tyr Phe Thr		
380	385	390
Phe Asn Pro His Phe Ile Ser Leu Pro Pro Ser Thr Pro Pro Thr		
395	400	405
Arg Val Gly Val Phe Leu Asp Tyr Glu Gly Gly Thr Ile Ser Phe		
410	415	420
Phe Asn Thr Asn Asp Gln Ser Leu Ile Tyr Thr Leu Leu Thr Cys		
425	430	435
Gln Phe Glu Gly Leu Leu Arg Pro Tyr Ile Gln His Ala Met Tyr		
440	445	450
Asp Glu Glu Lys Gly Thr Pro Ile Phe Ile Cys Pro Val Ser Trp		
455	460	465

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<210> 268
 <211> 2103
 <212> DNA
 <213> Homo sapiens

<400> 268
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<210> 269
<211> 423
<212> PRT
<213> Homo sapiens

<400> 269
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Val Leu Ala Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr
35 40 45
Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr
50 55 60
Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn
65 70 75
Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala
80 85 90
Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val
95 100 105
Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu
110 115 120
Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp
125 130 135
Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val
140 145 150
Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile
155 160 165
Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr
170 175 180
Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly
185 190 195
Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln
200 205 210

Trp Asp Gly Ser	His Arg Cys Gly Ala	Thr Leu Ile Asn Ala	Thr
215		220	225
Trp Leu Val Ser	Ala Ala His Cys Phe	Thr Thr Tyr Lys Asn	Pro
230		235	240
Ala Arg Trp Thr	Ala Ser Phe Gly Val	Thr Ile Lys Pro Ser	Lys
245		250	255
Met Lys Arg Gly	Leu Arg Arg Ile Ile	Val His Glu Lys Tyr	Lys
260		265	270
His Pro Ser His	Asp Tyr Asp Ile Ser	Leu Ala Glu Leu Ser	Ser
275		280	285
Pro Val Pro Tyr	Thr Asn Ala Val His	Arg Val Cys Leu Pro	Asp
290		295	300
Ala Ser Tyr Glu	Phe Gln Pro Gly Asp	Val Met Phe Val Thr	Gly
305		310	315
Phe Gly Ala Leu	Lys Asn Asp Gly Tyr	Ser Gln Asn His Leu	Arg
320		325	330
Gln Ala Gln Val	Thr Leu Ile Asp Ala	Thr Thr Cys Asn Glu	Pro
335		340	345
Gln Ala Tyr Asn	Asp Ala Ile Thr Pro	Arg Met Leu Cys Ala	Gly
350		355	360
Ser Leu Glu Gly	Lys Thr Asp Ala Cys	Gln Gly Asp Ser Gly	Gly
365		370	375
Pro Leu Val Ser	Ser Asp Ala Arg Asp	Ile Trp Tyr Leu Ala	Gly
380		385	390
Ile Val Ser Trp	Gly Asp Glu Cys Ala	Lys Pro Asn Lys Pro	Gly
395		400	405
Val Tyr Thr Arg	Val Thr Ala Leu Arg	Asp Trp Ile Thr Ser	Lys
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Thr Gly Ile

<210> 270

<211> 1170

<212> DNA

<213> Homo sapiens

<400> 270

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cagacgtcag ctggtggatt cccgctgcat caaggcctac ccactgtctc 150

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<210> 271

<211> 238

<212> PRT

<213> Homo sapiens

<400> 271

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			20					25					30	
Glu	Glu	Ala	Asp	Glu	Thr	Glu	Thr	Ala	Trp	Pro	Pro	Leu	Pro	Ala
			35					40					45	

Val	Pro	Cys	Asp	Tyr	Asp	His	Cys	Arg	His	Leu	Gln	Val	Pro	Cys	
				50					55					60	
Lys	Glu	Leu	Gln	Arg	Val	Gly	Pro	Ala	Ala	Cys	Leu	Cys	Pro	Gly	
				65					70					75	
Leu	Ser	Ser	Pro	Ala	Gln	Pro	Pro	Asp	Pro	Pro	Arg	Met	Gly	Glu	
				80					85					90	
Val	Arg	Ile	Ala	Ala	Glu	Glu	Gly	Arg	Ala	Val	Val	His	Trp	Cys	
				95					100					105	
Ala	Pro	Phe	Ser	Pro	Val	Leu	His	Tyr	Trp	Leu	Leu	Leu	Trp	Asp	
				110					115					120	
Gly	Ser	Glu	Ala	Ala	Gln	Lys	Gly	Pro	Pro	Leu	Asn	Ala	Thr	Val	
				125					130					135	
Arg	Arg	Ala	Glu	Leu	Lys	Gly	Leu	Lys	Pro	Gly	Gly	Ile	Tyr	Val	
				140					145					150	
Val	Cys	Val	Val	Ala	Ala	Asn	Glu	Ala	Gly	Ala	Ser	Arg	Val	Pro	
				155					160					165	
Gln	Ala	Gly	Gly	Glu	Gly	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Ala	Phe	
				170					175					180	
Gly	Pro	Cys	Ser	Arg	Leu	Ala	Val	Pro	Pro	Asn	Pro	Arg	Thr	Leu	
				185					190					195	
Val	His	Ala	Ala	Val	Gly	Val	Gly	Thr	Ala	Leu	Ala	Leu	Leu	Ser	
				200					205					210	
Cys	Ala	Ala	Leu	Val	Trp	His	Phe	Cys	Leu	Arg	Asp	Arg	Trp	Gly	
				215					220					225	
Cys	Pro	Arg	Arg	Ala	Ala	Ala	Arg	Ala	Ala	Gly	Ala	Leu			
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<210> 272

<211> 2397

<212> DNA

<213> Homo sapiens

<400> 272

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tgcccttggg agtaggatgt ggtgaaagga tggggcttct cccttacggg 200
gctcacaatg gccagagaag attccgtgaa gtgtctgcgc tgcctgctct 250
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<210> 273

<211> 305

<212> PRT

<213> Homo sapiens

<400> 273

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Ala	Leu	Asn	Leu	Leu	Phe	Trp	Leu	Met	Ser	Ile	Ser	Val	Leu	Ala
				20					25					30
Val	Ser	Ala	Trp	Met	Arg	Asp	Tyr	Leu	Asn	Asn	Val	Leu	Thr	Leu
				35					40					45
Thr	Ala	Glu	Thr	Arg	Val	Glu	Glu	Ala	Val	Ile	Leu	Thr	Tyr	Phe
				50					55					60
Pro	Val	Val	His	Pro	Val	Met	Ile	Ala	Val	Cys	Cys	Phe	Leu	Ile
				65					70					75
Ile	Val	Gly	Met	Leu	Gly	Tyr	Cys	Gly	Thr	Val	Lys	Arg	Asn	Leu
				80					85					90
Leu	Leu	Leu	Ala	Trp	Tyr	Phe	Gly	Ser	Leu	Leu	Val	Ile	Phe	Cys
				95					100					105
Val	Glu	Leu	Ala	Cys	Gly	Val	Trp	Thr	Tyr	Glu	Gln	Glu	Leu	Met
				110					115					120

Val	Pro	Val	Gln	Trp	Ser	Asp	Met	Val	Thr	Leu	Lys	Ala	Arg	Met	
				125					130					135	
Thr	Asn	Tyr	Gly	Leu	Pro	Arg	Tyr	Arg	Trp	Leu	Thr	His	Ala	Trp	
				140					145					150	
Asn	Phe	Phe	Gln	Arg	Glu	Phe	Lys	Cys	Cys	Gly	Val	Val	Tyr	Phe	
				155					160					165	
Thr	Asp	Trp	Leu	Glu	Met	Thr	Glu	Met	Asp	Trp	Pro	Pro	Asp	Ser	
				170					175					180	
Cys	Cys	Val	Arg	Glu	Phe	Pro	Gly	Cys	Ser	Lys	Gln	Ala	His	Gln	
				185					190					195	
Glu	Asp	Leu	Ser	Asp	Leu	Tyr	Gln	Glu	Gly	Cys	Gly	Lys	Lys	Met	
				200					205					210	
Tyr	Ser	Phe	Leu	Arg	Gly	Thr	Lys	Gln	Leu	Gln	Val	Leu	Arg	Phe	
				215					220					225	
Leu	Gly	Ile	Ser	Ile	Gly	Val	Thr	Gln	Ile	Leu	Ala	Met	Ile	Leu	
				230					235					240	
Thr	Ile	Thr	Leu	Leu	Trp	Ala	Leu	Tyr	Tyr	Asp	Arg	Arg	Glu	Pro	
				245					250					255	
Gly	Thr	Asp	Gln	Met	Met	Ser	Leu	Lys	Asn	Asp	Asn	Ser	Gln	His	
				260					265					270	
Leu	Ser	Cys	Pro	Ser	Val	Glu	Leu	Leu	Lys	Pro	Ser	Leu	Ser	Arg	
				275					280					285	
Ile	Phe	Glu	His	Thr	Ser	Met	Ala	Asn	Ser	Phe	Asn	Thr	His	Phe	
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Glu	Met	Glu	Glu	Leu											
				305											

<210> 274

<211> 2063

<212> DNA

<213> Homo sapiens

<400> 274

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<210> 275

<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

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Val	Lys	Pro	Leu	Arg	Lys	Pro	Arg	Ile	Pro	Met	Glu	Thr	Phe	Arg	20	25	30	
Lys	Val	Gly	Ile	Pro	Ile	Ile	Ile	Ala	Leu	Leu	Ser	Leu	Ala	Ser	35	40	45	
Ile	Ile	Ile	Val	Val	Val	Leu	Ile	Lys	Val	Ile	Leu	Asp	Lys	Tyr	50	55	60	
Tyr	Phe	Leu	Cys	Gly	Gln	Pro	Leu	His	Phe	Ile	Pro	Arg	Lys	Gln	65	70	75	
Leu	Cys	Asp	Gly	Glu	Leu	Asp	Cys	Pro	Leu	Gly	Glu	Asp	Glu	Glu	80	85	90	
His	Cys	Val	Lys	Ser	Phe	Pro	Glu	Gly	Pro	Ala	Val	Ala	Val	Arg	95	100	105	
Leu	Ser	Lys	Asp	Arg	Ser	Thr	Leu	Gln	Val	Leu	Asp	Ser	Ala	Thr	110	115	120	
Gly	Asn	Trp	Phe	Ser	Ala	Cys	Phe	Asp	Asn	Phe	Thr	Glu	Ala	Leu	125	130	135	
Ala	Glu	Thr	Ala	Cys	Arg	Gln	Met	Gly	Tyr	Ser	Arg	Ala	Val	Glu	140	145	150	
Ile	Gly	Pro	Asp	Gln	Asp	Leu	Asp	Val	Val	Glu	Ile	Thr	Glu	Asn	155	160	165	
Ser	Gln	Glu	Leu	Arg	Met	Arg	Asn	Ser	Ser	Gly	Pro	Cys	Leu	Ser	170	175	180	

Gly Ser Leu Val	Ser Leu His Cys Leu	Ala Cys Gly Lys Ser Leu	185	190	195
Lys Thr Pro Arg	Val Val Gly Gly Glu	Glu Ala Ser Val Asp Ser	200	205	210
Trp Pro Trp Gln	Val Ser Ile Gln Tyr	Asp Lys Gln His Val Cys	215	220	225
Gly Gly Ser Ile	Leu Asp Pro His Trp	Val Leu Thr Ala Ala His	230	235	240
Cys Phe Arg Lys	His Thr Asp Val Phe	Asn Trp Lys Val Arg Ala	245	250	255
Gly Ser Asp Lys	Leu Gly Ser Phe Pro	Ser Leu Ala Val Ala Lys	260	265	270
Ile Ile Ile Ile	Glu Phe Asn Pro Met	Tyr Pro Lys Asp Asn Asp	275	280	285
Ile Ala Leu Met	Lys Leu Gln Phe Pro	Leu Thr Phe Ser Gly Thr	290	295	300
Val Arg Pro Ile	Cys Leu Pro Phe Phe	Asp Glu Glu Leu Thr Pro	305	310	315
Ala Thr Pro Leu	Trp Ile Ile Gly Trp	Gly Phe Thr Lys Gln Asn	320	325	330
Gly Gly Lys Met	Ser Asp Ile Leu Leu	Gln Ala Ser Val Gln Val	335	340	345
Ile Asp Ser Thr	Arg Cys Asn Ala Asp	Asp Ala Tyr Gln Gly Glu	350	355	360
Val Thr Glu Lys	Met Met Cys Ala Gly	Ile Pro Glu Gly Gly Val	365	370	375
Asp Thr Cys Gln	Gly Asp Ser Gly Gly	Pro Leu Met Tyr Gln Ser	380	385	390
Asp Gln Trp His	Val Val Gly Ile Val	Ser Trp Gly Tyr Gly Cys	395	400	405
Gly Gly Pro Ser	Thr Pro Gly Val Tyr	Thr Lys Val Ser Ala Tyr	410	415	420
Leu Asn Trp Ile	Tyr Asn Val Trp Lys	Ala Glu Leu	425	430	

<210> 276
 <211> 3143
 <212> DNA
 <213> Homo sapiens

<400> 276

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<210> 277

<211> 761

<212> PRT

<213> Homo sapiens

<400> 277

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Leu	Phe	Leu	Phe	Gln	Leu	Leu	Gln	Leu	Leu	Leu	Pro	Thr	Thr	Thr	20	25	30	
Ala	Gly	Gly	Gly	Gly	Gln	Gly	Pro	Met	Pro	Arg	Val	Arg	Tyr	Tyr	35	40	45	
Ala	Gly	Asp	Glu	Arg	Arg	Ala	Leu	Ser	Phe	Phe	His	Gln	Lys	Gly	50	55	60	
Leu	Gln	Asp	Phe	Asp	Thr	Leu	Leu	Leu	Ser	Gly	Asp	Gly	Asn	Thr	65	70	75	
Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Ile	Leu	Ala	Leu	Asp	Ile	Gln	80	85	90	
Asp	Pro	Gly	Val	Pro	Arg	Leu	Lys	Asn	Met	Ile	Pro	Trp	Pro	Ala	95	100	105	
Ser	Asp	Arg	Lys	Lys	Ser	Glu	Cys	Ala	Phe	Lys	Lys	Lys	Ser	Asn	110	115	120	
Glu	Thr	Gln	Cys	Phe	Asn	Phe	Ile	Arg	Val	Leu	Val	Ser	Tyr	Asn	125	130	135	
Val	Thr	His	Leu	Tyr	Thr	Cys	Gly	Thr	Phe	Ala	Phe	Ser	Pro	Ala	140	145	150	
Cys	Thr	Phe	Ile	Glu	Leu	Gln	Asp	Ser	Tyr	Leu	Leu	Pro	Ile	Ser	155	160	165	
Glu	Asp	Lys	Val	Met	Glu	Gly	Lys	Gly	Gln	Ser	Pro	Phe	Asp	Pro	170	175	180	
Ala	His	Lys	His	Thr	Ala	Val	Leu	Val	Asp	Gly	Met	Leu	Tyr	Ser	185	190	195	

Gly Thr Met Asn	Asn Phe Leu Gly Ser	Glu Pro Ile Leu Met Arg
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Thr Leu Gly Ser	Gln Pro Val Leu Lys	Thr Asp Asn Phe Leu Arg
215		220 225
Trp Leu His His	Asp Ala Ser Phe Val	Ala Ala Ile Pro Ser Thr
230		235 240
Gln Val Val Tyr	Phe Phe Phe Glu Glu	Thr Ala Ser Glu Phe Asp
245		250 255
Phe Phe Glu Arg	Leu His Thr Ser Arg	Val Ala Arg Val Cys Lys
260		265 270
Asn Asp Val Gly	Gly Glu Lys Leu Leu	Gln Lys Lys Trp Thr Thr
275		280 285
Phe Leu Lys Ala	Gln Leu Leu Cys Thr	Gln Pro Gly Gln Leu Pro
290		295 300
Phe Asn Val Ile	Arg His Ala Val Leu	Leu Pro Ala Asp Ser Pro
305		310 315
Thr Ala Pro His	Ile Tyr Ala Val Phe	Thr Ser Gln Trp Gln Val
320		325 330
Gly Gly Thr Arg	Ser Ser Ala Val Cys	Ala Phe Ser Leu Leu Asp
335		340 345
Ile Glu Arg Val	Phe Lys Gly Lys Tyr	Lys Glu Leu Asn Lys Glu
350		355 360
Thr Ser Arg Trp	Thr Thr Tyr Arg Gly	Pro Glu Thr Asn Pro Arg
365		370 375
Pro Gly Ser Cys	Ser Val Gly Pro Ser	Ser Asp Lys Ala Leu Thr
380		385 390
Phe Met Lys Asp	His Phe Leu Met Asp	Glu Gln Val Val Gly Thr
395		400 405
Pro Leu Leu Val	Lys Ser Gly Val Glu	Tyr Thr Arg Leu Ala Val
410		415 420
Glu Thr Ala Gln	Gly Leu Asp Gly His	Ser His Leu Val Met Tyr
425		430 435
Leu Gly Thr Thr	Thr Gly Ser Leu His	Lys Ala Val Val Ser Gly
440		445 450
Asp Ser Ser Ala	His Leu Val Glu Glu	Ile Gln Leu Phe Pro Asp
455		460 465
Pro Glu Pro Val	Arg Asn Leu Gln Leu	Ala Pro Thr Gln Gly Ala
470		475 480

Val Phe Val Gly Phe Ser Gly Gly Val Trp Arg Val Pro Arg Ala	485	490	495
Asn Cys Ser Val Tyr Glu Ser Cys Val Asp Cys Val Leu Ala Arg	500	505	510
Asp Pro His Cys Ala Trp Asp Pro Glu Ser Arg Thr Cys Cys Leu	515	520	525
Leu Ser Ala Pro Asn Leu Asn Ser Trp Lys Gln Asp Met Glu Arg	530	535	540
Gly Asn Pro Glu Trp Ala Cys Ala Ser Gly Pro Met Ser Arg Ser	545	550	555
Leu Arg Pro Gln Ser Arg Pro Gln Ile Ile Lys Glu Val Leu Ala	560	565	570
Val Pro Asn Ser Ile Leu Glu Leu Pro Cys Pro His Leu Ser Ala	575	580	585
Leu Ala Ser Tyr Tyr Trp Ser His Gly Pro Ala Ala Val Pro Glu	590	595	600
Ala Ser Ser Thr Val Tyr Asn Gly Ser Leu Leu Leu Ile Val Gln	605	610	615
Asp Gly Val Gly Gly Leu Tyr Gln Cys Trp Ala Thr Glu Asn Gly	620	625	630
Phe Ser Tyr Pro Val Ile Ser Tyr Trp Val Asp Ser Gln Asp Gln	635	640	645
Thr Leu Ala Leu Asp Pro Glu Leu Ala Gly Ile Pro Arg Glu His	650	655	660
Val Lys Val Pro Leu Thr Arg Val Ser Gly Gly Ala Ala Leu Ala	665	670	675
Ala Gln Gln Ser Tyr Trp Pro His Phe Val Thr Val Thr Val Leu	680	685	690
Phe Ala Leu Val Leu Ser Gly Ala Leu Ile Ile Leu Val Ala Ser	695	700	705
Pro Leu Arg Ala Leu Arg Ala Arg Gly Lys Val Gln Gly Cys Glu	710	715	720
Thr Leu Arg Pro Gly Glu Lys Ala Pro Leu Ser Arg Glu Gln His	725	730	735
Leu Gln Ser Pro Lys Glu Cys Arg Thr Ser Ala Ser Asp Val Asp	740	745	750
Ala Asp Asn Asn Cys Leu Gly Thr Glu Val Ala	755	760	

<210> 278
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 278
ctgctggtga aatctggcgt ggag 24

<210> 279
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 279
gtctggtcct ggctgtccac ccag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 280
catcttgtca tgtacctggg aaccaccaca gggtcgctcc acaag 45

<210> 281
<211> 2320
<212> DNA
<213> Homo sapiens

<400> 281
aggggtccctt agccggggcg agggcgcgca gccaggctg agatccgcgg 50
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atctacagta ggtggaagcc attatctact gatggaccgg gtttctcaga 200
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ccttttatgc cagattttta aaaggaagaa aatcatatc aagttatcag 300
ttggcttgca cctgaagatc atcaaagaga atttaaaaag agttttgatt 350
tctttctgga agaaacttta ggtggcagag gaaaatttga aaacttatta 400
aatgttctag aatacttggc gttgcagtgc agtcattttt taaatagaaa 450

ggatatcatg gattccttaa agaatgagaa cttcgacatg gtgatagttg 500
aaacttttga ctactgtcct ttcctgattg ctgagaagct tgggaagcca 550
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 tgtgcttgag agttcagggc cggacacagg ctcacaggtc tccacattgg 2200
 gtccctgtct ctggtgcccc cagtgaagctc cttcttggtt gagcaggcat 2250
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 tctctcccca acctcactaa 2320

<210> 282
 <211> 523
 <212> PRT
 <213> Homo sapiens

<400> 282
 Met Ala Gly Gln Arg Val Leu Leu Leu Val Gly Phe Leu Leu Pro
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 Gly Val Leu Leu Ser Glu Ala Ala Lys Ile Leu Thr Ile Ser Thr
 20 25 30
 Val Gly Gly Ser His Tyr Leu Leu Met Asp Arg Val Ser Gln Ile
 35 40 45
 Leu Gln Asp His Gly His Asn Val Thr Met Leu Asn His Lys Arg
 50 55 60
 Gly Pro Phe Met Pro Asp Phe Lys Lys Glu Glu Lys Ser Tyr Gln
 65 70 75
 Val Ile Ser Trp Leu Ala Pro Glu Asp His Gln Arg Glu Phe Lys
 80 85 90
 Lys Ser Phe Asp Phe Phe Leu Glu Glu Thr Leu Gly Gly Arg Gly
 95 100 105
 Lys Phe Glu Asn Leu Leu Asn Val Leu Glu Tyr Leu Ala Leu Gln
 110 115 120
 Cys Ser His Phe Leu Asn Arg Lys Asp Ile Met Asp Ser Leu Lys
 125 130 135
 Asn Glu Asn Phe Asp Met Val Ile Val Glu Thr Phe Asp Tyr Cys
 140 145 150
 Pro Phe Leu Ile Ala Glu Lys Leu Gly Lys Pro Phe Val Ala Ile

155										160					165				
Leu	Ser	Thr	Ser	Phe	Gly	Ser	Leu	Glu	Phe	Gly	Leu	Pro	Ile	Pro					
				170					175					180					
Leu	Ser	Tyr	Val	Pro	Val	Phe	Arg	Ser	Leu	Leu	Thr	Asp	His	Met					
				185					190					195					
Asp	Phe	Trp	Gly	Arg	Val	Lys	Asn	Phe	Leu	Met	Phe	Phe	Ser	Phe					
				200					205					210					
Cys	Arg	Arg	Gln	Gln	His	Met	Gln	Ser	Thr	Phe	Asp	Asn	Thr	Ile					
				215					220					225					
Lys	Glu	His	Phe	Thr	Glu	Gly	Ser	Arg	Pro	Val	Leu	Ser	His	Leu					
				230					235					240					
Leu	Leu	Lys	Ala	Glu	Leu	Trp	Phe	Ile	Asn	Ser	Asp	Phe	Ala	Phe					
				245					250					255					
Asp	Phe	Ala	Arg	Pro	Leu	Leu	Pro	Asn	Thr	Val	Tyr	Val	Gly	Gly					
				260					265					270					
Leu	Met	Glu	Lys	Pro	Ile	Lys	Pro	Val	Pro	Gln	Asp	Leu	Glu	Asn					
				275					280					285					
Phe	Ile	Ala	Lys	Phe	Gly	Asp	Ser	Gly	Phe	Val	Leu	Val	Thr	Leu					
				290					295					300					
Gly	Ser	Met	Val	Asn	Thr	Cys	Gln	Asn	Pro	Glu	Ile	Phe	Lys	Glu					
				305					310					315					
Met	Asn	Asn	Ala	Phe	Ala	His	Leu	Pro	Gln	Gly	Val	Ile	Trp	Lys					
				320					325					330					
Cys	Gln	Cys	Ser	His	Trp	Pro	Lys	Asp	Val	His	Leu	Ala	Ala	Asn					
				335					340					345					
Val	Lys	Ile	Val	Asp	Trp	Leu	Pro	Gln	Ser	Asp	Leu	Leu	Ala	His					
				350					355					360					
Pro	Ser	Ile	Arg	Leu	Phe	Val	Thr	His	Gly	Gly	Gln	Asn	Ser	Ile					
				365					370					375					
Met	Glu	Ala	Ile	Gln	His	Gly	Val	Pro	Met	Val	Gly	Ile	Pro	Leu					
				380					385					390					
Phe	Gly	Asp	Gln	Pro	Glu	Asn	Met	Val	Arg	Val	Glu	Ala	Lys	Lys					
				395					400					405					
Phe	Gly	Val	Ser	Ile	Gln	Leu	Lys	Lys	Leu	Lys	Ala	Glu	Thr	Leu					
				410					415					420					
Ala	Leu	Lys	Met	Lys	Gln	Ile	Met	Glu	Asp	Lys	Arg	Tyr	Lys	Ser					
				425					430					435					
Ala	Ala	Val	Ala	Ala	Ser	Val	Ile	Leu	Arg	Ser	His	Pro	Leu	Ser					

440	445	450
Pro Thr Gln Arg Leu Val Gly Trp Ile	Asp His Val Leu Gln Thr	
455	460	465
Gly Gly Ala Thr His Leu Lys Pro Tyr	Val Phe Gln Gln Pro Trp	
470	475	480
His Glu Gln Tyr Leu Phe Asp Val Phe	Val Phe Leu Leu Gly Leu	
485	490	495
Thr Leu Gly Thr Leu Trp Leu Cys Gly	Lys Leu Leu Gly Met Ala	
500	505	510
Val Trp Trp Leu Arg Gly Ala Arg Lys	Val Lys Glu Thr	
515	520	

<210> 283
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 283
 tgcctttgct cacctacccc aagg 24

<210> 284
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 284
 tcaggctggt ctccaaagag aggg 24

<210> 285
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 285
 cccaaagatg tccacctggc tgcaaattgtg aaaattgtgg actgg 45

<210> 286
 <211> 2340
 <212> DNA
 <213> Homo sapiens

<400> 286
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ggttgagggg ctgcctctgg catatgcaca cactcacaca ttctgtcaca 100
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gtgctgtccc atccagcagg gctaccctga agctctggct gcagccctcc 200
cgtccagtgg gcaggcggct tcatccctcc tttctctccc aaagcccaac 250
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gagtaagagt gggaggcagg acagagctgg gacacaggta tggagagggg 350
gttcagcgag cctagagagg gcagactatc agggtgccgg cggtgagaat 400
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 agaggaaaat aaatatcaaa ctgtatacta aaattaaaaa 2340

<210> 287
 <211> 205
 <212> PRT
 <213> Homo sapiens

<400> 287
 Met Leu Gly Ala Lys Pro His Trp Leu Pro Gly Pro Leu His Ser
 1 5 10 15
 Pro Gly Leu Pro Leu Val Leu Val Leu Leu Ala Leu Gly Ala Gly
 20 25 30
 Trp Ala Gln Glu Gly Ser Glu Pro Val Leu Leu Glu Gly Glu Cys
 35 40 45
 Leu Val Val Cys Glu Pro Gly Arg Ala Ala Ala Gly Gly Pro Gly
 50 55 60
 Gly Ala Ala Leu Gly Glu Ala Pro Pro Gly Arg Val Ala Phe Ala
 65 70 75

Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn	
				80					85					90	
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu	
				95					100					105	
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val	
				110					115					120	
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn	
				125					130					135	
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val	
				140					145					150	
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala	
				155					160					165	
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser	
				170					175					180	
Leu	Arg	Leu	Arg	Arg	Gly	Asn	Leu	Leu	Gly	Gly	Trp	Lys	Tyr	Ser	
				185					190					195	
Ser	Phe	Ser	Gly	Phe	Leu	Ile	Phe	Pro	Leu						
				200					205						

<210> 288

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 288

aggcagccac cagctctgtg ctac 24

<210> 289

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 289

cagagaggga agatgaggaa gccagag 27

<210> 290

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 290
ctgtgctact gcccttggac cctggggacc gagtgtctct gc 42

<210> 291
<211> 1570
<212> DNA
<213> Homo sapiens

<400> 291
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 aaaaaaaaaa aaaaaaaaaa 1570

<210> 292

<211> 388

<212> PRT

<213> Homo sapiens

<400> 292

Met	Lys	Thr	Leu	Ile	Ala	Ala	Tyr	Ser	Gly	Val	Leu	Arg	Gly	Glu	1	5	10	15
Arg	Gln	Ala	Glu	Ala	Asp	Arg	Ser	Gln	Arg	Ser	His	Gly	Gly	Pro	20	25	30	
Ala	Leu	Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser	35	40	45	
Ile	Leu	Ser	Ala	Leu	Gln	Asp	Leu	Phe	Ser	Val	Thr	Trp	Leu	Asn	50	55	60	
Arg	Ser	Lys	Val	Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln	65	70	75	
Trp	Val	Leu	Ser	Phe	Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Ala	Ile	80	85	90	
Leu	Met	Tyr	Ile	Phe	Cys	Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu	95	100	105	
Tyr	Phe	Thr	Trp	Leu	Val	Phe	Asp	Trp	Asn	Thr	Pro	Lys	Lys	Gly	110	115	120	
Gly	Arg	Arg	Ser	Gln	Trp	Val	Arg	Asn	Trp	Ala	Val	Trp	Arg	Tyr	125	130	135	
Phe	Arg	Asp	Tyr	Phe	Pro	Ile	Gln	Leu	Val	Lys	Thr	His	Asn	Leu	140	145	150	
Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr	His	Pro	His	Gly	Ile	155	160	165	
Met	Gly	Leu	Gly	Ala	Phe	Cys	Asn	Phe	Ser	Thr	Glu	Ala	Thr	Glu	170	175	180	

Val Ser Lys Lys Phe Pro Gly Ile Arg Pro Tyr Leu Ala Thr Leu	185	190	195
Ala Gly Asn Phe Arg Met Pro Val Leu Arg Glu Tyr Leu Met Ser	200	205	210
Gly Gly Ile Cys Pro Val Ser Arg Asp Thr Ile Asp Tyr Leu Leu	215	220	225
Ser Lys Asn Gly Ser Gly Asn Ala Ile Ile Ile Val Val Gly Gly	230	235	240
Ala Ala Glu Ser Leu Ser Ser Met Pro Gly Lys Asn Ala Val Thr	245	250	255
Leu Arg Asn Arg Lys Gly Phe Val Lys Leu Ala Leu Arg His Gly	260	265	270
Ala Asp Leu Val Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr	275	280	285
Lys Gln Val Ile Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Gln	290	295	300
Lys Lys Phe Gln Lys Tyr Ile Gly Phe Ala Pro Cys Ile Phe His	305	310	315
Gly Arg Gly Leu Phe Ser Ser Asp Thr Trp Gly Leu Val Pro Tyr	320	325	330
Ser Lys Pro Ile Thr Thr Val Val Gly Glu Pro Ile Thr Ile Pro	335	340	345
Lys Leu Glu His Pro Thr Gln Gln Asp Ile Asp Leu Tyr His Thr	350	355	360
Met Tyr Met Glu Ala Leu Val Lys Leu Phe Asp Lys His Lys Thr	365	370	375
Lys Phe Gly Leu Pro Glu Thr Glu Val Leu Glu Val Asn	380	385	

<210> 293

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

gctgacctgg ttcccatcta ctcc 24

<210> 294

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cccacagaca cccatgacac ttcc 24

<210> 295

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 295

aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcttggggcc 50

<210> 296

<211> 3060

<212> DNA

<213> Homo sapiens

<400> 296

ggggcgccgg atgggggccg gggcgccgg gcgccgact cgctgaggcc 50

ccgacgcagg gccggggccg gccagggcc gaggagcgc gcggccagag 100

cggggccgcg gaggcgacgc cggggacgcc gcgcgcacga gcagggtggc 150

gcggctgcag gcttgtccag ccggaagccc tgagggcagc tgttcccact 200

ggctctgctg accttgtgcc ttggacggct gtcctcagcg aggggccgtg 250

caccgcctcc tgagcagcgc catgggcctg ctggccttcc tgaagacca 300

gttcgtgctg cacctgctgg tcggctttgt ctctgtgtg agtggctctg 350

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cagctctacc gccgcctcaa ctgccgcctc gcctactcac tctggagcca 450

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gcgcttcgga gtgctgggga gctccaaggt cctcgctaag aaggagctgc 650

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tgcaagcgga agtgggagga ggaccgggac accgtggtcg aagggtgag 750

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<210> 297

<211> 368

<212> PRT

<213> Homo sapiens

<400> 297

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Leu	Val	Gly	Phe	Val	Phe	Val	Val	Ser	Gly	Leu	Val	Ile	Asn	Phe
				20					25					30
Val	Gln	Leu	Cys	Thr	Leu	Ala	Leu	Trp	Pro	Val	Ser	Lys	Gln	Leu
				35					40					45
Tyr	Arg	Arg	Leu	Asn	Cys	Arg	Leu	Ala	Tyr	Ser	Leu	Trp	Ser	Gln
				50					55					60
Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Cys	Thr	Glu	Cys	Thr	Leu
				65					70					75
Phe	Thr	Asp	Gln	Ala	Thr	Val	Glu	Arg	Phe	Gly	Lys	Glu	His	Ala

80										85					90				
Val	Ile	Ile	Leu	Asn	His	Asn	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly					
				95					100					105					
Trp	Thr	Met	Cys	Glu	Arg	Phe	Gly	Val	Leu	Gly	Ser	Ser	Lys	Val					
				110					115					120					
Leu	Ala	Lys	Lys	Glu	Leu	Leu	Tyr	Val	Pro	Leu	Ile	Gly	Trp	Thr					
				125					130					135					
Trp	Tyr	Phe	Leu	Glu	Ile	Val	Phe	Cys	Lys	Arg	Lys	Trp	Glu	Glu					
				140					145					150					
Asp	Arg	Asp	Thr	Val	Val	Glu	Gly	Leu	Arg	Arg	Leu	Ser	Asp	Tyr					
				155					160					165					
Pro	Glu	Tyr	Met	Trp	Phe	Leu	Leu	Tyr	Cys	Glu	Gly	Thr	Arg	Phe					
				170					175					180					
Thr	Glu	Thr	Lys	His	Arg	Val	Ser	Met	Glu	Val	Ala	Ala	Ala	Lys					
				185					190					195					
Gly	Leu	Pro	Val	Leu	Lys	Tyr	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly					
				200					205					210					
Phe	Thr	Thr	Ala	Val	Lys	Cys	Leu	Arg	Gly	Thr	Val	Ala	Ala	Val					
				215					220					225					
Tyr	Asp	Val	Thr	Leu	Asn	Phe	Arg	Gly	Asn	Lys	Asn	Pro	Ser	Leu					
				230					235					240					
Leu	Gly	Ile	Leu	Tyr	Gly	Lys	Lys	Tyr	Glu	Ala	Asp	Met	Cys	Val					
				245					250					255					
Arg	Arg	Phe	Pro	Leu	Glu	Asp	Ile	Pro	Leu	Asp	Glu	Lys	Glu	Ala					
				260					265					270					
Ala	Gln	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Leu	Gln					
				275					280					285					
Glu	Ile	Tyr	Asn	Gln	Lys	Gly	Met	Phe	Pro	Gly	Glu	Gln	Phe	Lys					
				290					295					300					
Pro	Ala	Arg	Arg	Pro	Trp	Thr	Leu	Leu	Asn	Phe	Leu	Ser	Trp	Ala					
				305					310					315					
Thr	Ile	Leu	Leu	Ser	Pro	Leu	Phe	Ser	Phe	Val	Leu	Gly	Val	Phe					
				320					325					330					
Ala	Ser	Gly	Ser	Pro	Leu	Leu	Ile	Leu	Thr	Phe	Leu	Gly	Phe	Val					
				335					340					345					
Gly	Ala	Ala	Ser	Phe	Gly	Val	Arg	Arg	Leu	Ile	Gly	Glu	Ser	Leu					
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 298
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<210> 299
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 299
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<210> 300
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 300
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<210> 301
 <211> 1334
 <212> DNA
 <213> Homo sapiens

<400> 301
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<210> 302

<211> 143

<212> PRT

<213> Homo sapiens

<400> 302

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His	Leu	Cys	Val	Cys	Phe	Ser	Phe	Ala	Leu	Ala	Leu	Gly	His	Phe
				20				25						30
Leu	Leu	Ile	Ser	Leu	Val	Gly	Lys	Gly	Leu	Ser	Leu	Ser	Cys	Gly
				35				40						45
Val	Gly	Gly	Arg	Gln	Ala	Gly	Leu	Arg	Leu	Ile	Arg	Pro	Trp	Val
				50				55						60
Arg	Arg	Glu	Gly	Lys	Ile	Asn	Phe	Tyr	Thr	Asn	Gly	Asp	Ser	Trp

	65		70		75
Gly Leu Arg Pro Ala Ser Ser Val Lys Phe Leu Gly Ser Ala Tyr					
	80		85		90
Thr Phe Phe Ser Leu Thr Trp His Thr Leu Leu Lys Ala Ser Gln					
	95		100		105
Gly Phe Ser Leu Phe Leu Gly Ser Lys Tyr Leu Glu Leu Gln Glu					
	110		115		120
Pro Ser Trp Ser Gly Pro Cys Pro Pro Gly Gln Leu His Cys Thr					
	125		130		135
Cys Gly Val Leu Leu Ser Phe Leu					
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<210> 303

<211> 1768

<212> DNA

<213> Homo sapiens

<400> 303

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<210> 304

<211> 109

<212> PRT

<213> Homo sapiens

<400> 304

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Val	Phe	Cys	Ser	Leu	Val	Thr	Ser	Leu	Tyr	Leu	Pro	Asn	Thr	Glu
				20					25					30
Asp	Leu	Ser	Leu	Trp	Leu	Trp	Pro	Lys	Pro	Asp	Leu	His	Ser	Gly
				35					40					45
Thr	Arg	Thr	Glu	Val	Ser	Thr	His	Thr	Val	Pro	Ser	Lys	Pro	Gly
				50					55					60
Thr	Ala	Ser	Pro	Cys	Trp	Pro	Leu	Ala	Gly	Ala	Val	Pro	Ser	Pro

	65		70		75
Thr Val Ser Arg	Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala				
	80		85		90
Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly					
	95		100		105
Arg Arg Arg Asp					

<210> 305
 <211> 989
 <212> DNA
 <213> Homo sapiens

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<210> 306

<211> 262

<212> PRT

<213> Homo sapiens

<400> 306

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Leu	Gly	Ser	Ala	Ala	Leu	Gly	Ala	Ala	Phe	Ala	Thr	Gly	Leu	Phe
				20					25					30
Leu	Gly	Arg	Arg	Cys	Pro	Pro	Trp	Arg	Gly	Arg	Arg	Glu	Gln	Cys
				35					40					45
Leu	Leu	Pro	Pro	Glu	Asp	Ser	Arg	Leu	Trp	Gln	Tyr	Leu	Leu	Ser
				50					55					60
Arg	Ser	Met	Arg	Glu	His	Pro	Ala	Leu	Arg	Ser	Leu	Arg	Leu	Leu
				65					70					75
Thr	Leu	Glu	Gln	Pro	Gln	Gly	Asp	Ser	Met	Met	Thr	Cys	Glu	Gln
				80					85					90
Ala	Gln	Leu	Leu	Ala	Asn	Leu	Ala	Arg	Leu	Ile	Gln	Ala	Lys	Lys
				95					100					105
Ala	Leu	Asp	Leu	Gly	Thr	Phe	Thr	Gly	Tyr	Ser	Ala	Leu	Ala	Leu
				110					115					120
Ala	Leu	Ala	Leu	Pro	Ala	Asp	Gly	Arg	Val	Val	Thr	Cys	Glu	Val
				125					130					135
Asp	Ala	Gln	Pro	Pro	Glu	Leu	Gly	Arg	Pro	Leu	Trp	Arg	Gln	Ala
				140					145					150
Glu	Ala	Glu	His	Lys	Ile	Asp	Leu	Arg	Leu	Lys	Pro	Ala	Leu	Glu
				155					160					165
Thr	Leu	Asp	Glu	Leu	Leu	Ala	Ala	Gly	Glu	Ala	Gly	Thr	Phe	Asp
				170					175					180
Val	Ala	Val	Val	Asp	Ala	Asp	Lys	Glu	Asn	Cys	Ser	Ala	Tyr	Tyr
				185					190					195
Glu	Arg	Cys	Leu	Gln	Leu	Leu	Arg	Pro	Gly	Gly	Ile	Leu	Ala	Val
				200					205					210
Leu	Arg	Val	Leu	Trp	Arg	Gly	Lys	Val	Leu	Gln	Pro	Pro	Lys	Gly
				215					220					225
Asp	Val	Ala	Ala	Glu	Cys	Val	Arg	Asn	Leu	Asn	Glu	Arg	Ile	Arg
				230					235					240
Arg	Asp	Val	Arg	Val	Tyr	Ile	Ser	Leu	Leu	Pro	Leu	Gly	Asp	Gly
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Leu Thr Leu Ala Phe Lys Ile
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<210> 307

<211> 2272

<212> DNA

<213> Homo sapiens

<400> 307

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<212> DNA

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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<210> 315

<211> 370

<212> PRT

<213> Homo sapiens

<400> 315

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Gln	Arg	Leu	Glu	Gln	Arg	Arg	Gln	Gln	Ala	Ser	Glu	Arg	Glu	Ala
				35					40					45
Pro	Ser	Ile	Glu	Gln	Arg	Leu	Gln	Glu	Val	Arg	Glu	Ser	Ile	Arg
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Arg	Ala	Gln	Val	Ser	Gln	Val	Lys	Gly	Ala	Ala	Arg	Leu	Ala	Leu
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Leu	Gln	Gly	Ala	Gly	Leu	Asp	Val	Glu	Arg	Trp	Leu	Lys	Pro	Ala
				80					85					90
Met	Thr	Gln	Ala	Gln	Asp	Glu	Val	Glu	Gln	Glu	Arg	Arg	Leu	Ser
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Glu	Ala	Arg	Leu	Ser	Gln	Arg	Asp	Leu	Ser	Pro	Thr	Ala	Glu	Asp
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Ala	Glu	Leu	Ser	Asp	Phe	Glu	Glu	Cys	Glu	Glu	Thr	Gly	Glu	Leu
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Phe	Glu	Glu	Pro	Ala	Pro	Gln	Ala	Leu	Ala	Thr	Arg	Ala	Leu	Pro
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Cys	Pro	Ala	His	Val	Val	Phe	Arg	Tyr	Gln	Ala	Gly	Arg	Glu	Asp	
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Glu	Leu	Thr	Ile	Thr	Glu	Gly	Glu	Trp	Leu	Glu	Val	Ile	Glu	Glu	
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Gln	Met	Leu	Pro	Ser	Pro	Ser	Pro	Pro	Ser	Phe	Ser	Pro	Pro	Ala	
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Asp	Lys	Ala	Leu	Asp	Phe	Pro	Gly	Phe	Leu	Asp	Met	Met	Ala	Pro	
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Arg	Leu	Arg	Pro	Met	Arg	Pro	Pro	Pro	Pro	Pro	Pro	Ala	Lys	Ala	
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<210> 316

<211> 4407

<212> DNA

<213> Homo sapiens

<400> 316

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<210> 317

<211> 837

<212> PRT

<213> Homo sapiens

<400> 317

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Leu	Ser	Trp	Leu	Val	Trp	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Ser	Leu	
				35					40					45	
Leu	Pro	Ser	Ala	Arg	Leu	Ala	Ser	Pro	Leu	Pro	Arg	Glu	Glu	Glu	
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Ile	Val	Phe	Pro	Glu	Lys	Leu	Asn	Gly	Ser	Val	Leu	Pro	Gly	Ser	
				65					70					75	
Gly	Ala	Pro	Ala	Arg	Leu	Leu	Cys	Arg	Leu	Gln	Ala	Phe	Gly	Glu	
				80					85					90	
Thr	Leu	Leu	Leu	Glu	Leu	Glu	Gln	Asp	Ser	Gly	Val	Gln	Val	Glu	
				95					100					105	
Gly	Leu	Thr	Val	Gln	Tyr	Leu	Gly	Gln	Ala	Pro	Glu	Leu	Leu	Gly	
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Gly	Ala	Glu	Pro	Gly	Thr	Tyr	Leu	Thr	Gly	Thr	Ile	Asn	Gly	Asp	
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Pro	Glu	Ser	Val	Ala	Ser	Leu	His	Trp	Asp	Gly	Gly	Ala	Leu	Leu	
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Gly	Val	Leu	Gln	Tyr	Arg	Gly	Ala	Glu	Leu	His	Leu	Gln	Pro	Leu	
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Glu	Gly	Gly	Thr	Pro	Asn	Ser	Ala	Gly	Gly	Pro	Gly	Ala	His	Ile	
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Leu	Arg	Arg	Lys	Ser	Pro	Ala	Ser	Gly	Gln	Gly	Pro	Met	Cys	Asn	
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Val	Lys	Ala	Pro	Leu	Gly	Ser	Pro	Ser	Pro	Arg	Pro	Arg	Arg	Ala	
				200					205					210	
Lys	Arg	Phe	Ala	Ser	Leu	Ser	Arg	Phe	Val	Glu	Thr	Leu	Val	Val	
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Ala	Asp	Asp	Lys	Met	Ala	Ala	Phe	His	Gly	Ala	Gly	Leu	Lys	Arg	
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Tyr	Leu	Leu	Thr	Val	Met	Ala	Ala	Ala	Ala	Lys	Ala	Phe	Lys	His	

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Ala Gln Thr Leu	Arg 290	Ser Phe Cys Ala	Trp 295	Gln Arg Gly Leu	Asn 300
Thr Pro Glu Asp	Ser 305	Gly Pro Asp His	Phe 310	Asp Thr Ala Ile	Leu 315
Phe Thr Arg Gln	Asp 320	Leu Cys Gly Val	Ser 325	Thr Cys Asp Thr	Leu 330
Gly Met Ala Asp	Val 335	Gly Thr Val Cys	Asp 340	Pro Ala Arg Ser	Cys 345
Ala Ile Val Glu	Asp 350	Asp Gly Leu Gln	Ser 355	Ala Phe Thr Ala	Ala 360
His Glu Leu Gly	His 365	Val Phe Asn Met	Leu 370	His Asp Asn Ser	Lys 375
Pro Cys Ile Ser	Leu 380	Asn Gly Pro Leu	Ser 385	Thr Ser Arg His	Val 390
Met Ala Pro Val	Met 395	Ala His Val Asp	Pro 400	Glu Glu Pro Trp	Ser 405
Pro Cys Ser Ala	Arg 410	Phe Ile Thr Asp	Phe 415	Leu Asp Asn Gly	Tyr 420
Gly His Cys Leu	Leu 425	Asp Lys Pro Glu	Ala 430	Pro Leu His Leu	Pro 435
Val Thr Phe Pro	Gly 440	Lys Asp Tyr Asp	Ala 445	Asp Arg Gln Cys	Gln 450
Leu Thr Phe Gly	Pro 455	Asp Ser Arg His	Cys 460	Pro Gln Leu Pro	Pro 465
Pro Cys Ala Ala	Leu 470	Trp Cys Ser Gly	His 475	Leu Asn Gly His	Ala 480
Met Cys Gln Thr	Lys 485	His Ser Pro Trp	Ala 490	Asp Gly Thr Pro	Cys 495
Gly Pro Ala Gln	Ala 500	Cys Met Gly Gly	Arg 505	Cys Leu His Met	Asp 510
Gln Leu Gln Asp	Phe 515	Asn Ile Pro Gln	Ala 520	Gly Gly Trp Gly	Pro 525
Trp Gly Pro Trp	Gly	Asp Cys Ser Arg	Thr	Cys Gly Gly Gly	Val

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<210> 318

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 318

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<210> 319

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 319

ctgtgctctt cggtgcagcc agtc 24

<210> 320

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 320

ccacagatgt ggtactgcct ggggcagtca gcttgcgcta cag 43

<210> 321

<211> 1197

<212> DNA

<213> Homo sapiens

<400> 321

cagcagtggc ctctcagtc tctcaaagca aggaaagagt actgtgtgct 50

gagagaccat ggcaaagaat cctccagaga attgtgaaga ctgtcacatt 100

ctaaatgcag aagcttttaa atccaagaaa atatgtaaat cacttaagat 150

ttgtggactg gtgttttgta tcttgccct aactctaatt gtctgtttt 200

gggggagcaa gcacttctgg ccggaggtag ccaaaaaagc ctatgacatg 250

gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300

tgatcctgtg accagaactg aaatattcag aagcggaat ggactgatg 350

aaacattgga agtgcacgac tttaaaaacg gatacactgg catctacttc 400
 gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga 450
 attttctgaa ccagaagagg aaatagatga gaatgaagaa attaccacaa 500
 ctttctttga acagtcagtg atttgggtcc cagcagaaaa gcctattgaa 550
 aaccgagatt ttcttaaaaa ttccaaaatt ctggagattt gtgataacgt 600
 gaccatgtat tggatcaatc ccactcta atcagtttct gagttacaag 650
 actttgagga ggaggagaa gatcttcact ttcttgccaa cgaaaaaaaa 700
 gggattgaac aaaatgaaca gtgggtggc cctcaagtga aagtagagaa 750
 gacccgtcac gccagacaag caagtgagga agaacttcca ataatgact 800
 atactgaaaa tggaatagaa ttgatccca tgctggatga gagaggttat 850
 tgttgtatct actgccgtcg aggcaaccgc tattgccgcc gcgtctgtga 900
 acctttacta ggctactacc catatccata ctgctaccaa ggaggacgag 950
 tcatctgtcg tgtcatcatg ccttgtaact ggtgggtggc ccgcatgctg 1000
 gggagggtct aataggaggt ttgagctcaa atgcttaaac tgctggcaac 1050
 atataataaa tgcatgctat tcaatgaatt tctgcctatg aggcactctg 1100
 cccttggtag ccagctctcc agaattactt gtaggtaatt cctctcttca 1150
 tgttctaata aacttctaca ttatcaccaa aaaaaaaaaa aaaaaaa 1197

<210> 322

<211> 317

<212> PRT

<213> Homo sapiens

<400> 322

Met	Ala	Lys	Asn	Pro	Pro	Glu	Asn	Cys	Glu	Asp	Cys	His	Ile	Leu
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Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys
				20					25					30
Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val
				35					40					45
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys
				50					55					60
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys
				65					70					75
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe

80								85				90			
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe	
				95					100					105	
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys	
				110					115					120	
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro	
				125					130					135	
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe	
				140					145					150	
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn	
				155					160					165	
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn	
				170					175					180	
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu	
				185					190					195	
Leu	Gln	Asp	Phe	Glu	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala	
				200					205					210	
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro	
				215					220					225	
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu	
				230					235					240	
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe	
				245					250					255	
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg	
				260					265					270	
Arg	Gly	Asn	Arg	Tyr	Cys	Arg	Arg	Val	Cys	Glu	Pro	Leu	Leu	Gly	
				275					280					285	
Tyr	Tyr	Pro	Tyr	Pro	Tyr	Cys	Tyr	Gln	Gly	Gly	Arg	Val	Ile	Cys	
				290					295					300	
Arg	Val	Ile	Met	Pro	Cys	Asn	Trp	Trp	Val	Ala	Arg	Met	Leu	Gly	
				305					310					315	

Arg Val

<210> 323

<211> 1174

<212> DNA

<213> Homo sapiens

<400> 323

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 ggccgtgcag cttctgggct tcctgctcag cttcctgggc atgggtgggca 150
 cgttgatcac caccatcctg ccgcactggc ggaggacagc gcacgtgggc 200
 accaacaatcc tcacggccgt gtcctacctg aaagggctct ggatggagtg 250
 tgtgtggcac agcacaggca tctaccagtg ccagatctac cgatccctgc 300
 tggcgctgcc ccaagacctc caggctgccc gcgccctcat ggtcatctcc 350
 tgctgtctct cgggcatagc ctgcgcctgc gccgtcatcg ggatgaagtg 400
 cacgcgtgc gccaaaggga caccgcgcaa gaccaccttt gccatcctcg 450
 gcggcaccct cttcatcctg gccggcctcc tgtgcatggt ggccgtctcc 500
 tggaccacca acgacgtggt gcagaacttc tacaaccgc tgctgccag 550
 cggcatgaag tttgagattg gccaggccct gtacctgggc ttcattctct 600
 cgtccctctc gctcattggt ggacacctgc tttgcctgtc ctgccaggac 650
 gaggcaccct acaggcccta ccaggccccg ccaggggcca ccacgaccac 700
 tgcaaacacc gcacctgcct accagccacc agctgcctac aaagacaatc 750
 gggccccctc agtgacctcg gccacgcaca gcgggtacag gctgaacgac 800
 tacgtgtgag tccccacagc ctgcttctcc cctgggctgc tgtgggctgg 850
 gtccccggcg ggactgtcaa tggaggcagg ggttcacagca caaagtttac 900
 ttctgggcaa tttttgtatc caaggaaata atgtgaatgc gaggaatgt 950
 ctttagagca caggacaga gggggaaata agaggaggag aaagctctct 1000
 ataccaaaga ctgaaaaaaaa aaatcctgtc tgtttttgta tttattatat 1050
 atatttatgt ggggtgatttg ataacaagtt taatataaag tgacttggga 1100
 gtttggtcag tggggttggt ttgtgatcca ggaataaacc ttgcggatgt 1150
 ggctgtttat gaaaaaaaaa aaaa 1174

<210> 324

<211> 239

<212> PRT

<213> Homo sapiens

<400> 324

Met	Ala	Ser	Thr	Ala	Val	Gln	Leu	Leu	Gly	Phe	Leu	Leu	Ser	Phe
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Leu Gly Met Val Gly Thr Leu Ile Thr Thr Ile Leu Pro His Trp

20										25					30				
Arg	Arg	Thr	Ala	His	Val	Gly	Thr	Asn	Ile	Leu	Thr	Ala	Val	Ser					
				35					40					45					
Tyr	Leu	Lys	Gly	Leu	Trp	Met	Glu	Cys	Val	Trp	His	Ser	Thr	Gly					
				50					55					60					
Ile	Tyr	Gln	Cys	Gln	Ile	Tyr	Arg	Ser	Leu	Leu	Ala	Leu	Pro	Gln					
				65					70					75					
Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Met	Val	Ile	Ser	Cys	Leu	Leu					
				80					85					90					
Ser	Gly	Ile	Ala	Cys	Ala	Cys	Ala	Val	Ile	Gly	Met	Lys	Cys	Thr					
				95					100					105					
Arg	Cys	Ala	Lys	Gly	Thr	Pro	Ala	Lys	Thr	Thr	Phe	Ala	Ile	Leu					
				110					115					120					
Gly	Gly	Thr	Leu	Phe	Ile	Leu	Ala	Gly	Leu	Leu	Cys	Met	Val	Ala					
				125					130					135					
Val	Ser	Trp	Thr	Thr	Asn	Asp	Val	Val	Gln	Asn	Phe	Tyr	Asn	Pro					
				140					145					150					
Leu	Leu	Pro	Ser	Gly	Met	Lys	Phe	Glu	Ile	Gly	Gln	Ala	Leu	Tyr					
				155					160					165					
Leu	Gly	Phe	Ile	Ser	Ser	Ser	Leu	Ser	Leu	Ile	Gly	Gly	Thr	Leu					
				170					175					180					
Leu	Cys	Leu	Ser	Cys	Gln	Asp	Glu	Ala	Pro	Tyr	Arg	Pro	Tyr	Gln					
				185					190					195					
Ala	Pro	Pro	Arg	Ala	Thr	Thr	Thr	Thr	Ala	Asn	Thr	Ala	Pro	Ala					
				200					205					210					
Tyr	Gln	Pro	Pro	Ala	Ala	Tyr	Lys	Asp	Asn	Arg	Ala	Pro	Ser	Val					
				215					220					225					
Thr	Ser	Ala	Thr	His	Ser	Gly	Tyr	Arg	Leu	Asn	Asp	Tyr	Val						
				230					235										

<210> 325

<211> 2121

<212> DNA

<213> Homo sapiens

<400> 325

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gcatcgcggc caccgggatg gacatgtgga gcaccaggga cctgtacgac 200

aaccccgta cctccgtgtt ccagtagaa gggctctgga ggagctgcgt 250
gaggcagagt tcaggcttca ccgaatgcag gccctatttc accatcctgg 300
gacttccagc catgctgcag gcagtgcgag ccctgatgat cgtaggcata 350
gtcctgggtg ccattggcct cctgggtatcc atctttgccc tgaaatgcat 400
ccgcattggc agcatggagg actctgcaa agccaacatg aactgacct 450
ccgggatcat gttcattgtc tcaggctctt gtgcaattgc tggagtgtct 500
gtgtttgcca acatgctggt gactaacttc tggatgtcca cagctaacat 550
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gggggtgtga tgatgtgcat cgctgccgg ggctggcac cagaagaaac 700
caactacaaa gccgtttctt atcatgcctc aggccacagt gttgcctaca 750
agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac 800
aagaagatat acgatggagg tgccgcaca gaggacgagg tacaatttta 850
tccttcaaag cagactatg tgtaatgctc taagacctct cagcacgggc 900
ggaagaaact cccggagagc tcacccaaaa aacaaggaga tcccatctag 950
atttcttctt gcttttgact cacagctgga agttagaaaa gcctcgattt 1000
catctttgga gaggccaaat ggtcttagcc tcagtctctg tctctaaata 1050
ttccaccata aaacagctga gttatttatg aattagaggc tatagctcac 1100
attttcaatc ctctatttct ttttttaaat ataactttct actctgatga 1150
gagaatgtgg ttttaatctc tctctcacat tttgatgatt tagacagact 1200
ccccctcttc ctctagtca ataaacccat tgatgatcta tttcccagct 1250
tatccccaag aaaacttttg aaaggaaaga gtagaccaa agatgttatt 1300
ttctgctggt tgaattttgt cccccaccc ccaacttggc tagtaataaa 1350
cacttactga agaagaagca ataagagaaa gatatttgta atctctccag 1400
cccatgatct cggttttctt aactgtgat cttaaaagt accaaaccaa 1450
agtcattttc agtttgaggc aaccaaacct ttctactgct gttgacatct 1500
tcttattaca gcaacacat tctaggagtt tcctgagctc tccactggag 1550
tcctctttct gtcgcggtc agaaattgtc cctagatgaa tgagaaaatt 1600

atttttttta atttaagtcc taaatatagt taaaataaat aatgttttag 1650
 taaaatgata cactatctct gtgaaatagc ctcaccccta catgtggata 1700
 gaaggaaatg aaaaaataat tgctttgaca ttgtctatat ggtactttgt 1750
 aaagtcatgc ttaagtacaa attccatgaa aagctcacac ctgtaatcct 1800
 agcactttgg gaggctgagg aggaaggatc acttgagccc agaagttcga 1850
 gactagcctg ggcaacatgg agaagccctg tctctacaaa atacagagag 1900
 aaaaaatcag ccagtcatgg tggcatacac ctgtagtccc agcattccgg 1950
 gaggctgagg tgggaggatc acttgagccc agggagggtg gggctgcagt 2000
 gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050
 gtctaaaaaa ataaaaaata aataatggaa cacagcaagt cctaggaagt 2100
 aggttaaaac taattcttta a 2121

<210> 326

<211> 261

<212> PRT

<213> Homo sapiens

<400> 326

Met	Ser	Thr	Thr	Thr	Cys	Gln	Val	Val	Ala	Phe	Leu	Leu	Ser	Ile
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Leu	Gly	Leu	Ala	Gly	Cys	Ile	Ala	Ala	Thr	Gly	Met	Asp	Met	Trp
				20					25					30
Ser	Thr	Gln	Asp	Leu	Tyr	Asp	Asn	Pro	Val	Thr	Ser	Val	Phe	Gln
				35					40					45
Tyr	Glu	Gly	Leu	Trp	Arg	Ser	Cys	Val	Arg	Gln	Ser	Ser	Gly	Phe
				50					55					60
Thr	Glu	Cys	Arg	Pro	Tyr	Phe	Thr	Ile	Leu	Gly	Leu	Pro	Ala	Met
				65					70					75
Leu	Gln	Ala	Val	Arg	Ala	Leu	Met	Ile	Val	Gly	Ile	Val	Leu	Gly
				80					85					90
Ala	Ile	Gly	Leu	Leu	Val	Ser	Ile	Phe	Ala	Leu	Lys	Cys	Ile	Arg
				95					100					105
Ile	Gly	Ser	Met	Glu	Asp	Ser	Ala	Lys	Ala	Asn	Met	Thr	Leu	Thr
				110					115					120
Ser	Gly	Ile	Met	Phe	Ile	Val	Ser	Gly	Leu	Cys	Ala	Ile	Ala	Gly
				125					130					135
Val	Ser	Val	Phe	Ala	Asn	Met	Leu	Val	Thr	Asn	Phe	Trp	Met	Ser
				140					145					150

Thr	Ala	Asn	Met	Tyr	Thr	Gly	Met	Gly	Gly	Met	Val	Gln	Thr	Val
				155						160				165
Gln	Thr	Arg	Tyr	Thr	Phe	Gly	Ala	Ala	Leu	Phe	Val	Gly	Trp	Val
				170						175				180
Ala	Gly	Gly	Leu	Thr	Leu	Ile	Gly	Gly	Val	Met	Met	Cys	Ile	Ala
				185						190				195
Cys	Arg	Gly	Leu	Ala	Pro	Glu	Glu	Thr	Asn	Tyr	Lys	Ala	Val	Ser
				200						205				210
Tyr	His	Ala	Ser	Gly	His	Ser	Val	Ala	Tyr	Lys	Pro	Gly	Gly	Phe
				215						220				225
Lys	Ala	Ser	Thr	Gly	Phe	Gly	Ser	Asn	Thr	Lys	Asn	Lys	Lys	Ile
				230						235				240
Tyr	Asp	Gly	Gly	Ala	Arg	Thr	Glu	Asp	Glu	Val	Gln	Ser	Tyr	Pro
				245						250				255
Ser	Lys	His	Asp	Tyr	Val									
				260										

<210> 327
 <211> 2010
 <212> DNA
 <213> Homo sapiens

<400> 327
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 caacccatgc cttagaaatc gctgggctgt ttcttggtgg tgttggaatg 150
 gtgggcacag tggctgtcac tgtcatgcct cagtggagag tgtcggcctt 200
 cattgaaaac aacatcgtgg tttttgaaaa cttctgggaa ggactgtgga 250
 tgaattgcgt gaggcaggct aacatcagga tgcagtgcaa aatctatgat 300
 tccctgctgg ctctttctcc ggacctacag gcagccagag gactgatgtg 350
 tgctgcttcc gtgatgtcct tcttggtctt catgatggcc atccttggca 400
 tgaaatgcac caggtgcacg ggggacaatg agaagtgaa ggctcacatt 450
 ctgctgacgg ctggaatcat cttcatcatc acgggcatgg tgggtgctcat 500
 ccctgtgagc tgggttgcca atgccatcat cagagatttc tataactcaa 550
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 tggaccacgg cactggtgct gattgttgga ggagctctgt tctgctgcgt 650

tttttgttgc aacgaaaaga gcagtagcta cagatactcg ataccttccc 700
 atcgcacaac ccaaaaaagt tatcacaccg gaaagáagtc accgagcgtc 750
 tactccagaa gtcagtatgt gtagtttgtgt atgttttttt aactttacta 800
 taaagccatg caaatgacaa aaatctatat tacttttctca aaatggaccc 850
 caaagaaaact ttgattttact gttcttaact gcctaattctt aattacagga 900
 actgtgcatc agctatttat gattctataa gctatttcag cagaatgaga 950
 tattaacccc aatgctttga ttgttctaga aagtatagta atttgttttc 1000
 taagggtggtt caagcatcta ctcttttttat catttacttc aaaatgacat 1050
 tgctaaagac tgcattattt tactactgta atttctccac gacatagcat 1100
 tatgtacata gatgagtgtg acatttatat ctccataga gacatgctta 1150
 tatgggtttta tttaaaatga aatgccagtc cattacactg aataaataga 1200
 actcaactat tgcttttcag ggaaatcatg gatagggttg aagaaggtta 1250
 ctattaattg tttaaaaaca gcttagggat taatgtcctc catttataat 1300
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 gttttaggaa agtgaaaata tttttgtttt tgtatttgaa gaagaatgat 1600
 gcattttgac aagaaatcat atatgtatgg atatatttta ataagtattt 1650
 gagtacagac tttgaggttt catcaatata aataaaagag cagaaaaata 1700
 tgtcttggtt ttcatttgct taccaaaaaa acaacaacaa aaaaagttgt 1750
 cctttgagaa cttcacctgc tcctatgtgg gtacctgagt caaaattgtc 1800
 atttttgttc tgtgaaaaat aaatttcctt cttgtaccat ttctgttttag 1850
 ttttactaaa atctgtaaat actgtatttt tctgtttatt ccaaatttga 1900
 tgaaactgac aatccaattt gaaagtttgt gtcgacgtct gtctagctta 1950
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<211> 225
<212> PRT
<213> Homo sapiens

<400> 328

Met	Ala	Thr	His	Ala	Leu	Glu	Ile	Ala	Gly	Leu	Phe	Leu	Gly	Gly	
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Val	Gly	Met	Val	Gly	Thr	Val	Ala	Val	Thr	Val	Met	Pro	Gln	Trp	
				20					25					30	
Arg	Val	Ser	Ala	Phe	Ile	Glu	Asn	Asn	Ile	Val	Val	Phe	Glu	Asn	
				35					40					45	
Phe	Trp	Glu	Gly	Leu	Trp	Met	Asn	Cys	Val	Arg	Gln	Ala	Asn	Ile	
				50					55					60	
Arg	Met	Gln	Cys	Lys	Ile	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Ser	Pro	
				65					70					75	
Asp	Leu	Gln	Ala	Ala	Arg	Gly	Leu	Met	Cys	Ala	Ala	Ser	Val	Met	
				80					85					90	
Ser	Phe	Leu	Ala	Phe	Met	Met	Ala	Ile	Leu	Gly	Met	Lys	Cys	Thr	
				95					100					105	
Arg	Cys	Thr	Gly	Asp	Asn	Glu	Lys	Val	Lys	Ala	His	Ile	Leu	Leu	
				110					115					120	
Thr	Ala	Gly	Ile	Ile	Phe	Ile	Ile	Thr	Gly	Met	Val	Val	Leu	Ile	
				125					130					135	
Pro	Val	Ser	Trp	Val	Ala	Asn	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	
				140					145					150	
Ser	Ile	Val	Asn	Val	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Glu	Ala	Leu	
				155					160					165	
Tyr	Leu	Gly	Trp	Thr	Thr	Ala	Leu	Val	Leu	Ile	Val	Gly	Gly	Ala	
				170					175					180	
Leu	Phe	Cys	Cys	Val	Phe	Cys	Cys	Asn	Glu	Lys	Ser	Ser	Ser	Tyr	
				185					190					195	
Arg	Tyr	Ser	Ile	Pro	Ser	His	Arg	Thr	Thr	Gln	Lys	Ser	Tyr	His	
				200					205					210	
Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val	
				215					220					225	

<210> 329
<211> 1315
<212> DNA
<213> Homo sapiens

<400> 329

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 gaccgctttc atcggcaaca gcatcgtggt ggcccaggtg gtgtgggagg 150
 gcctgtggat gtctgctgtg gtgcagagca ccggccagat gcagtgcaag 200
 gtgtacgact cactgctggc gctgccacag gacctgcagg ctgcacgtgc 250
 cctctgtgtc atcgccctcc ttgtggccct gttcggcttg ctggtctacc 300
 ttgtgtgggc caagtgtacc acctgtgtgg aggagaagga ttccaaggcc 350
 cgcttgtgc tcacctctgg gattgtcttt gtcattctcag gggtcctgac 400
 gctaataccc gtgtgctgga cggcgcatgc catcatccgg gacttctata 450
 accccctggg ggctgaggcc caaaagcggg agctgggggc ctccctctac 500
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 gctactcaac atctgcccct gccatctctc gggggccctc tgagtaccct 650
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 gctgcccccc atcctactca ggtctctgga gtcctctctc tcaccctgg 1100
 aaaaacaaat catctgttaa caaaggactg cccacctccg gaacttctga 1150
 cctctgtttc ctccgtcctg ataagacgtc cccccccag ggccagggtcc 1200
 cagctatgta gacccccgcc cccacctcca aactgcacc cttctgcct 1250
 gccccctcg tctaccccc tttacactca catttttatc aaataaagca 1300
 tgttttgtta gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ser	Ala	Gly	Met	Gln	Ile	Leu	Gly	Val	Val	Leu	Thr	Leu
1				5					10					15
Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp
				20					25					30
Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val
				35					40					45
Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly
				50					55					60
Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln
				65					70					75
Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val
				80					85					90
Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr
				95					100					105
Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr
				110					115					120
Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro
				125					130					135
Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro
				140					145					150
Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Tyr
				155					160					165
Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Leu	Gly	Gly	Gly	Leu
				170					175					180
Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His
				185					190					195
Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly
				200					205					210
Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val					
				215					220					

<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331

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ttctacatct tgagcatctt ctaccactcc gaattgaacc agtcttcaaa 100

gtaaaggcaa tggcatttta tcccttgcaa attgctgggc tggttcttgg 150
 gttccttggc atgggtggga ctcttgccac aacccttctg cctcagtggg 200
 ggagtatcag cttttgttgg cagcaacatt attgtctttg agaggctctg 250
 ggaagggctc tggatgaatt gcatccgaca agccagggtc cggttgcaat 300
 gcaagttcta tagctccttg ttggctctcc cgcctgccct ggaaacagcc 350
 cgggccctca tgtgtgtggc tgttgctctc tccttgatcg ccctgcttat 400
 tggcatctgt ggcatagaag aggtccagtg cacaggctct aacgagaggg 450
 ccaaagcata ccttctggga acttcaggag tcctcttcat cctgacgggt 500
 atcttcgttc tgattccggt gagctggaca gccaatataa tcatcagaga 550
 tttctacaac ccagccatcc acataggtca gaaacgagag ctgggagcag 600
 cacttttcct tggctgggca agcgtgctg tcctcttcat tggagggggg 650
 ctgctttgtg gatcttgctg ctgcaacaga aagaagcaag ggtacagata 700
 tccagtgcct ggctaccgtg tgccacacac agataagcga agaaatacga 750
 caatgcttag taagacctcc accagttagt tctaatagcct ccttttggct 800
 ccaagtatgg actatggtca atgtttttta taaagtctg ctagaaactg 850
 taagtatgtg aggcaggaga acttgcttta tgtctagatt tacattgata 900
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 acattctgac ttcaggtgta ttaaatgcat tgactattgt tggacccaat 1000
 cgctgctcca attttcatat tctaaattca agtataacca taatcattag 1050
 caagtgtaca atgatggact acttattact ttttgacat catgtattat 1100
 ctgataagaa tctaaagttg aaattgatat tctataacaa taaaacatat 1150
 acctattcta 1160

<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met	Asn	Cys	Ile	Arg	Gln	Ala	Arg	Val	Arg	Leu	Gln	Cys	Lys	Phe
1				5					10					15

Tyr	Ser	Ser	Leu	Leu	Ala	Leu	Pro	Pro	Ala	Leu	Glu	Thr	Ala	Arg
			20						25					30

Ala Leu Met Cys Val Ala Val Ala Leu Ser Leu Ile Ala Leu Leu

	35		40		45
Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn					
	50		55		60
Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe					
	65		70		75
Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala					
	80		85		90
Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly					
	95		100		105
Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser					
	110		115		120
Ala Ala Val Leu Phe Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys					
	125		130		135
Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly					
	140		145		150
Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu					
	155		160		165
Ser Lys Thr Ser Thr Ser Tyr Val					
	170				

<210> 333

<211> 535

<212> DNA

<213> Homo sapiens

<400> 333

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ctcagaagct gctagtctgt ctccaaaaaa agtggactgc agcatTTaca 150
agaagtatcc agtggTggcc atccctgcc ccatcacata cctaccagtt 200
tgtggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccga 250
gagcttgaaa agtaatggaa gagttcagtt tcttcacgat ggaagttgct 300
aaattctcca tggacataga gagaaaggaa tgatattctc atcatcatct 350
tcatcatccc aggctctgac tgagtttctt tcagttttac tgatgttctg 400
ggTgggggac agagccagat tcagagtaat cttgactgaa tggagaaagt 450
ttctgtgcta cccctacaaa cccatgcctc actgacagac cagcattttt 500
tttttaacac gtcaataaaa aaataatctc ccaga 535

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<210> 334
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 334

Met	Lys	Ile	Thr	Gly	Gly	Leu	Leu	Leu	Leu	Cys	Thr	Val	Val	Tyr
1				5					10					15
Phe	Cys	Ser	Ser	Ser	Glu	Ala	Ala	Ser	Leu	Ser	Pro	Lys	Lys	Val
				20					25					30
Asp	Cys	Ser	Ile	Tyr	Lys	Lys	Tyr	Pro	Val	Val	Ala	Ile	Pro	Cys
				35					40					45
Pro	Ile	Thr	Tyr	Leu	Pro	Val	Cys	Gly	Ser	Asp	Tyr	Ile	Thr	Tyr
				50					55					60
Gly	Asn	Glu	Cys	His	Leu	Cys	Thr	Glu	Ser	Leu	Lys	Ser	Asn	Gly
				65					70					75
Arg	Val	Gln	Phe	Leu	His	Asp	Gly	Ser	Cys					
				80					85					

<210> 335
 <211> 742
 <212> DNA
 <213> Homo sapiens

<400> 335

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ctgctcgcgc cccgccgcca tggctgcctc ccccgcgcg cctgctgtcc 100
tggccctgac cgggctggcg ctgctcctgc tcctgtgctg gggcccaggt 150
ggcataagtg gaaataaact caagctgatg cttcaaaaac gagaagcacc 200
tggtccaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250
tccttggcag cctgaagcgc cagaagcggc agctgtggga ccggactcgg 300
cccgaggtgc agcagtggta ccagcagttt ctctacatgg gctttgatga 350
agcgaaattt gaagatgaca tcacctattg gcttaacaga gatcgaaatg 400
gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450
gcaattggtc cccggagccc ctacggcttt aggcattggag ccagcgtcaa 500
ctacgatgac tactaaccat gacttgccac acgctgtaca agaagcaa at 550
agcgattctc ttcattgtat tcctaattgcc ttacactact tggttttctga 600
tttgctctat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650
gaagagttaa aacaacacat gtaaattgcct tttgatattt catgggaatg 700

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cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336

<211> 148

<212> PRT

<213> Homo sapiens

<400> 336

Met	Ala	Ala	Ser	Pro	Ala	Arg	Pro	Ala	Val	Leu	Ala	Leu	Thr	Gly	
1				5					10					15	
Leu	Ala	Leu	Leu	Leu	Leu	Leu	Cys	Trp	Gly	Pro	Gly	Gly	Ile	Ser	
				20					25					30	
Gly	Asn	Lys	Leu	Lys	Leu	Met	Leu	Gln	Lys	Arg	Glu	Ala	Pro	Val	
				35					40					45	
Pro	Thr	Lys	Thr	Lys	Val	Ala	Val	Asp	Glu	Asn	Lys	Ala	Lys	Glu	
				50					55					60	
Phe	Leu	Gly	Ser	Leu	Lys	Arg	Gln	Lys	Arg	Gln	Leu	Trp	Asp	Arg	
				65					70					75	
Thr	Arg	Pro	Glu	Val	Gln	Gln	Trp	Tyr	Gln	Gln	Phe	Leu	Tyr	Met	
				80					85					90	
Gly	Phe	Asp	Glu	Ala	Lys	Phe	Glu	Asp	Asp	Ile	Thr	Tyr	Trp	Leu	
				95					100					105	
Asn	Arg	Asp	Arg	Asn	Gly	His	Glu	Tyr	Tyr	Gly	Asp	Tyr	Tyr	Gln	
				110					115					120	
Arg	His	Tyr	Asp	Glu	Asp	Ser	Ala	Ile	Gly	Pro	Arg	Ser	Pro	Tyr	
				125					130					135	
Gly	Phe	Arg	His	Gly	Ala	Ser	Val	Asn	Tyr	Asp	Asp	Tyr			
				140					145						

<210> 337

<211> 1310

<212> DNA

<213> Homo sapiens

<400> 337

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tgaaggggtg ggtgatgagg tgaccgtcct tttctcggtg cttgctgcc 150

ttctgggtgct ggcccttgcc tgggtctcaa cgcacaccgc tgagggcggg 200

gaccactgc ccagccgctc agggacccca acgcatccc agcccagcgc 250

agccatggca gctaccgaca gcatgagagg ggaggcccca ggggcagaga 300

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ccccagcct gagacacaga ggtcaagctg cacagccaga gccagcacg 350
gggttcacag caacaccgcc agccccggac tccccgcagg agccctcgt 400
gctacggctg aaattcctca atgattcaga gcagggtggc agggcctggc 450
cccacgacac cattggctcc ttgaaaagga cccagtttcc cggccgggaa 500
cagcagggtgc gactcatcta ccaagggcag ctgctaggcg acgacacca 550
gacctgggc agccttcacc tccctcccaa ctgcgttctc cactgccacg 600
tgtccacgag agtcggtccc ccaaateccc cctgcccgcc ggggtccgag 650
cccgccctt cggggctgga aatcggcagc ctgctgctgc ccctgctgct 700
cctgctggtg ctgctgctct ggtactgcca gatccagtac cggcccttct 750
ttccctgac cgccactctg ggctggccg gcttcacct gctcctcagt 800
ctcctggcct ttgccatgta ccgccgtag tgcctccgcg ggcgcttggc 850
agcgtcgccg gccctcccg accttgctcc ccgcgcgcg gcgggagctg 900
ctgcctgcc aggccgcct ctccggcctg cctcttcccg ctgccctgga 950
gccagccct gcgcgcgaga ggactcccgg gactggcgga ggccccgcc 1000
tgcgaccgcc ggggctcggg gccacctccc ggggctgctg aacctcagcc 1050
cgcactggga gtgggtcct cggggtcggg catctgctgt cgctgcctcg 1100
gccccgggca gagccgggcc gccccggggg ccggtcttag tgttctgccg 1150
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acgccaggtc ggtgggaggc tgggaaggg gagcggggag gggcagagga 1250
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aaaaaaaaa 1310

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<210> 338

<211> 246

<212> PRT

<213> Homo sapiens

<400> 338

Met	Thr	Leu	Ile	Glu	Gly	Val	Gly	Asp	Glu	Val	Thr	Val	Leu	Phe
1				5					10					15

Ser	Val	Leu	Ala	Cys	Leu	Leu	Val	Leu	Ala	Leu	Ala	Trp	Val	Ser
				20					25					30

Thr	His	Thr	Ala	Glu	Gly	Gly	Asp	Pro	Leu	Pro	Gln	Pro	Ser	Gly
				35					40					45

Thr	Pro	Thr	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Met	Ala	Ala	Thr	Asp	
				50					55					60	
Ser	Met	Arg	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Thr	Pro	Ser	Leu	Arg	
				65					70					75	
His	Arg	Gly	Gln	Ala	Ala	Gln	Pro	Glu	Pro	Ser	Thr	Gly	Phe	Thr	
				80					85					90	
Ala	Thr	Pro	Pro	Ala	Pro	Asp	Ser	Pro	Gln	Glu	Pro	Leu	Val	Leu	
				95					100					105	
Arg	Leu	Lys	Phe	Leu	Asn	Asp	Ser	Glu	Gln	Val	Ala	Arg	Ala	Trp	
				110					115					120	
Pro	His	Asp	Thr	Ile	Gly	Ser	Leu	Lys	Arg	Thr	Gln	Phe	Pro	Gly	
				125					130					135	
Arg	Glu	Gln	Gln	Val	Arg	Leu	Ile	Tyr	Gln	Gly	Gln	Leu	Leu	Gly	
				140					145					150	
Asp	Asp	Thr	Gln	Thr	Leu	Gly	Ser	Leu	His	Leu	Pro	Pro	Asn	Cys	
				155					160					165	
Val	Leu	His	Cys	His	Val	Ser	Thr	Arg	Val	Gly	Pro	Pro	Asn	Pro	
				170					175					180	
Pro	Cys	Pro	Pro	Gly	Ser	Glu	Pro	Gly	Pro	Ser	Gly	Leu	Glu	Ile	
				185					190					195	
Gly	Ser	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
				200					205					210	
Trp	Tyr	Cys	Gln	Ile	Gln	Tyr	Arg	Pro	Phe	Phe	Pro	Leu	Thr	Ala	
				215					220					225	
Thr	Leu	Gly	Leu	Ala	Gly	Phe	Thr	Leu	Leu	Leu	Ser	Leu	Leu	Ala	
				230					235					240	
Phe	Ala	Met	Tyr	Arg	Pro										
				245											

<210> 339

<211> 849

<212> DNA

<213> Homo sapiens

<400> 339

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atgacaaagg cgctactcat ctatttggtc agcagctttc ttgccctaaa 200

tcaggccagc ctcacagtc gctgtgactt ggcccaggtg ctgcagctgg 250

aggacttgga tgggtttgag gggtactccc tgagtgactg gctgtgcctg 300
 gcttttgtgg aaagcaagtt caacatatca aagataaatg aaaatgcgga 350
 tggaagcttt gactatggcc tcttccagat caacagccac tactggtgca 400
 acgattataa gagttactcg gaaaaccttt gccacgtaga ctgtcaagat 450
 ctgtgaatc ccaaccttct tgcaggcatc cactgcgcaa aaaggattgt 500
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 ggattcttca tttcttcttc ctactgcctc cacttcatgt tatittcttc 700
 ccttcccatt tacaactaaa actgaccaga gccccaggaa taaatggttt 750
 tcttggttc ctccttactc ccactctggac ccagtcccct ggttcctgtc 800
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<210> 340

<211> 148

<212> PRT

<213> Homo sapiens

<400> 340

Met	Thr	Lys	Ala	Leu	Leu	Ile	Tyr	Leu	Val	Ser	Ser	Phe	Leu	Ala	1	5	10	15
Leu	Asn	Gln	Ala	Ser	Leu	Ile	Ser	Arg	Cys	Asp	Leu	Ala	Gln	Val	20	25	30	
Leu	Gln	Leu	Glu	Asp	Leu	Asp	Gly	Phe	Glu	Gly	Tyr	Ser	Leu	Ser	35	40	45	
Asp	Trp	Leu	Cys	Leu	Ala	Phe	Val	Glu	Ser	Lys	Phe	Asn	Ile	Ser	50	55	60	
Lys	Ile	Asn	Glu	Asn	Ala	Asp	Gly	Ser	Phe	Asp	Tyr	Gly	Leu	Phe	65	70	75	
Gln	Ile	Asn	Ser	His	Tyr	Trp	Cys	Asn	Asp	Tyr	Lys	Ser	Tyr	Ser	80	85	90	
Glu	Asn	Leu	Cys	His	Val	Asp	Cys	Gln	Asp	Leu	Leu	Asn	Pro	Asn	95	100	105	
Leu	Leu	Ala	Gly	Ile	His	Cys	Ala	Lys	Arg	Ile	Val	Ser	Gly	Ala	110	115	120	
Arg	Gly	Met	Asn	Asn	Trp	Val	Glu	Trp	Arg	Leu	His	Cys	Ser	Gly	125	130	135	

Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg
140 145

<210> 341

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 341

ccctccaagg atgacaaagg cgc 23

<210> 342

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 342

ggtcagcagc tttcttgccc taaatcagg 29

<210> 343

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 343

atctcaggcg gcatcctgtc agcc 24

<210> 344

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 344

gtggatgcct gcaagaaggt tggg 24

<210> 345

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 345

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<210> 346

<211> 2575

<212> DNA

<213> Homo sapiens

<400> 346

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actgagaacc caccagctca tcccagacac ctcatagcaa cctatttata 100
caaaggggga aagaaacacc tgagcagaat ggaatcatta tttttttccc 150
aaggagaaaa ccggggtaaa gggaggggaag caattcaatt tgaagtcctt 200
gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250
ggggtgaaac ttgggtcctg tggttttctg attgtaagtg gaagcaggtc 300
ttgcacacgc tgttggcaaa tgtcaggacc aggttaagtg actggcagaa 350
aaacttccag gtggaacaag caacccatgt tctgctgcaa gcttgaagga 400
gcctggagcg ggagaaagct aacttgaaca tgacctgttg catttgga 450
gttctagcaa catgctccta aggaagcgat acaggcacag accatgcaga 500
ctccagttcc tctgctgct cctgatgctg ggatgcgtcc tgatgatggt 550
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aagccagcaa gcacagccct gaagccagggt accgcctgga ctttggggaa 650
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cccaaagagg gactgggggg ctgatgagga cggggagggtg tctgaagaag 900
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 tcagcagaat agctggtgac aggagccgag tggatatctcc ggtgatagat 1400
 gtgattgact ggaagacttt ccagtattac ccctcaaagg acctgcagcg 1450
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 atgtgaggaa ggccctccag tccccataa gcccacatcag gagccctgtg 1550
 gtgcccggag aggtggtggc catggacaga cattacttcc aaaacactgg 1600
 agcgtatgac tctcttatgt cgctgcgagg tggtgaaaac ctggaactgt 1650
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<210> 347

<211> 639

<212> PRT
<213> Homo sapiens

<400> 347

Met	Leu	Leu	Arg	Lys	Arg	Tyr	Arg	His	Arg	Pro	Cys	Arg	Leu	Gln	
1				5					10					15	
Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Gly	Cys	Val	Leu	Met	Met	Val	
				20					25					30	
Ala	Met	Leu	His	Pro	Pro	His	His	Thr	Leu	His	Gln	Thr	Val	Thr	
				35					40					45	
Ala	Gln	Ala	Ser	Lys	His	Ser	Pro	Glu	Ala	Arg	Tyr	Arg	Leu	Asp	
				50					55					60	
Phe	Gly	Glu	Ser	Gln	Asp	Trp	Val	Leu	Glu	Ala	Glu	Asp	Glu	Gly	
				65					70					75	
Glu	Glu	Tyr	Ser	Pro	Leu	Glu	Gly	Leu	Pro	Pro	Phe	Ile	Ser	Leu	
				80					85					90	
Arg	Glu	Asp	Gln	Leu	Leu	Val	Ala	Val	Ala	Leu	Pro	Gln	Ala	Arg	
				95					100					105	
Arg	Asn	Gln	Ser	Gln	Gly	Arg	Arg	Gly	Gly	Ser	Tyr	Arg	Leu	Ile	
				110					115					120	
Lys	Gln	Pro	Arg	Arg	Gln	Asp	Lys	Glu	Ala	Pro	Lys	Arg	Asp	Trp	
				125					130					135	
Gly	Ala	Asp	Glu	Asp	Gly	Glu	Val	Ser	Glu	Glu	Glu	Glu	Leu	Thr	
				140					145					150	
Pro	Phe	Ser	Leu	Asp	Pro	Arg	Gly	Leu	Gln	Glu	Ala	Leu	Ser	Ala	
				155					160					165	
Arg	Ile	Pro	Leu	Gln	Arg	Ala	Leu	Pro	Glu	Val	Arg	His	Pro	Leu	
				170					175					180	
Cys	Leu	Gln	Gln	His	Pro	Gln	Asp	Ser	Leu	Pro	Thr	Ala	Ser	Val	
				185					190					195	
Ile	Leu	Cys	Phe	His	Asp	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr	
				200					205					210	
Val	His	Ser	Ile	Leu	Asp	Thr	Val	Pro	Arg	Ala	Phe	Leu	Lys	Glu	
				215					220					225	
Ile	Ile	Leu	Val	Asp	Asp	Leu	Ser	Gln	Gln	Gly	Gln	Leu	Lys	Ser	
				230					235					240	
Ala	Leu	Ser	Glu	Tyr	Val	Ala	Arg	Leu	Glu	Gly	Val	Lys	Leu	Leu	
				245					250					255	
Arg	Ser	Asn	Lys	Arg	Leu	Gly	Ala	Ile	Arg	Ala	Arg	Met	Leu	Gly	
				260					265					270	

Ala Thr Arg Ala Thr Gly Asp Val Leu Val Phe Met Asp Ala His	275	280	285
Cys Glu Cys His Pro Gly Trp Leu Glu Pro Leu Leu Ser Arg Ile	290	295	300
Ala Gly Asp Arg Ser Arg Val Val Ser Pro Val Ile Asp Val Ile	305	310	315
Asp Trp Lys Thr Phe Gln Tyr Tyr Pro Ser Lys Asp Leu Gln Arg	320	325	330
Gly Val Leu Asp Trp Lys Leu Asp Phe His Trp Glu Pro Leu Pro	335	340	345
Glu His Val Arg Lys Ala Leu Gln Ser Pro Ile Ser Pro Ile Arg	350	355	360
Ser Pro Val Val Pro Gly Glu Val Val Ala Met Asp Arg His Tyr	365	370	375
Phe Gln Asn Thr Gly Ala Tyr Asp Ser Leu Met Ser Leu Arg Gly	380	385	390
Gly Glu Asn Leu Glu Leu Ser Phe Lys Ala Trp Leu Cys Gly Gly	395	400	405
Ser Val Glu Ile Leu Pro Cys Ser Arg Val Gly His Ile Tyr Gln	410	415	420
Asn Gln Asp Ser His Ser Pro Leu Asp Gln Glu Ala Thr Leu Arg	425	430	435
Asn Arg Val Arg Ile Ala Glu Thr Trp Leu Gly Ser Phe Lys Glu	440	445	450
Thr Phe Tyr Lys His Ser Pro Glu Ala Phe Ser Leu Ser Lys Ala	455	460	465
Glu Lys Pro Asp Cys Met Glu Arg Leu Gln Leu Gln Arg Arg Leu	470	475	480
Gly Cys Arg Thr Phe His Trp Phe Leu Ala Asn Val Tyr Pro Glu	485	490	495
Leu Tyr Pro Ser Glu Pro Arg Pro Ser Phe Ser Gly Lys Leu His	500	505	510
Asn Thr Gly Leu Gly Leu Cys Ala Asp Cys Gln Ala Glu Gly Asp	515	520	525
Ile Leu Gly Cys Pro Met Val Leu Ala Pro Cys Ser Asp Ser Arg	530	535	540
Gln Gln Gln Tyr Leu Gln His Thr Ser Arg Lys Glu Ile His Phe	545	550	555

Gly	Ser	Pro	Gln	His	Leu	Cys	Phe	Ala	Val	Arg	Gln	Glu	Gln	Val	560	565	570
Ile	Leu	Gln	Asn	Cys	Thr	Glu	Glu	Gly	Leu	Ala	Ile	His	Gln	Gln	575	580	585
His	Trp	Asp	Phe	Gln	Glu	Asn	Gly	Met	Ile	Val	His	Ile	Leu	Ser	590	595	600
Gly	Lys	Cys	Met	Glu	Ala	Val	Val	Gln	Glu	Asn	Asn	Lys	Asp	Leu	605	610	615
Tyr	Leu	Arg	Pro	Cys	Asp	Gly	Lys	Ala	Arg	Gln	Gln	Trp	Arg	Phe	620	625	630
Asp	Gln	Ile	Asn	Ala	Val	Asp	Glu	Arg							635		

<210> 348

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 348

ggagaggtgg tggccatgga cag 23

<210> 349

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 349

ctgtcactgc aaggagccaa cacc 24

<210> 350

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 350

tatgtcgtg cgaggtggtg aaaacctcga actgtctttc aaggc 45

<210> 351

<211> 2524

<212> DNA

<213> Homo sapiens

<400> 351

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ctcagacatg gagtccagga tgtggcctgc gctgctgctg tcccacctcc 100
tccctctctg gccactgctg ttgctgcccc tcccaccgcc tgctcagggc 150
tcttcattcct cccctcgaac cccaccagcc ccagcccgcc ccccgctgtgc 200
caggggaggg ccctcgcccc cacgtcatgt gtgcgtgtgg gagcgagcac 250
ctccaccaag ccgatctcct cgggtcccaa gatcacgtcg gcaagtcttg 300
cctggcactg cccccccagc cccccatca ggctttgagg aggggccgcc 350
ctcatcccaa taccctggg ctatcgtgtg gggcccacc gtgtctcgag 400
aggatggagg ggaccccaac tctgccaatc ccggatttct ggactatggg 450
tttgagccc ctcatgggct cgcaacccca ccccccaact cagactccat 500
gcgaggtgat ggagatgggc ttatccttgg agaggcacct gccaccctgc 550
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gtcacaatta ccattccat catcattgtt ctctgggcca ctggcatcat 650
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 tcaaataaag cctttgcaag ataa 2524

<210> 352

<211> 243

<212> PRT

<213> Homo sapiens

<400> 352

Met	Arg	Pro	Gln	Gly	Pro	Ala	Ala	Ser	Pro	Gln	Arg	Leu	Arg	Gly
1				5					10					15

Leu	Leu	Leu	Leu	Leu	Leu	Leu	Gln	Leu	Pro	Ala	Pro	Ser	Ser	Ala
				20					25					30

Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg	35	40	45
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala	50	55	60
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro	65	70	75
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys	80	85	90
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn	95	100	105
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu	110	115	120
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser	125	130	135
Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	140	145	150
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	155	160	165
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	170	175	180
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	185	190	195
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	200	205	210
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	215	220	225
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	230	235	240

Leu Pro Lys

<210> 353

<211> 480

<212> DNA

<213> Homo sapiens

<400> 353

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cggccaggat ggcacacctgt ctggccctgc gcattggcgct gctgctggtc 100

tccgggggttc tggccctgc ggtgctcaca gacgatgttc cacaggagcc 150

cgtgcccacg ctgtggaacg agccggccga gctgccgtcg ggagaaggcc 200
 ccgtggagag caccagcccc ggccgggagc ccgtggacac cggccccca 250
 gccccacccg tcgcgccagg acccgaggac agcaccgcgc aggagcggct 300
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 tcgccgccct gctggccacc tgcgtggtgc tggcgctcgt ggtcgtcgcg 400
 ctgagaaagt tttctgcctc ctgaagcgaa taaaggggcc gcgcccggcc 450
 gcggcgcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354

<211> 121

<212> PRT

<213> Homo sapiens

<400> 354

Met	Ala	Ser	Cys	Leu	Ala	Leu	Arg	Met	Ala	Leu	Leu	Leu	Val	Ser
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Gly	Val	Leu	Ala	Pro	Ala	Val	Leu	Thr	Asp	Asp	Val	Pro	Gln	Glu
				20					25					30
Pro	Val	Pro	Thr	Leu	Trp	Asn	Glu	Pro	Ala	Glu	Leu	Pro	Ser	Gly
				35					40					45
Glu	Gly	Pro	Val	Glu	Ser	Thr	Ser	Pro	Gly	Arg	Glu	Pro	Val	Asp
				50					55					60
Thr	Gly	Pro	Pro	Ala	Pro	Thr	Val	Ala	Pro	Gly	Pro	Glu	Asp	Ser
				65					70					75
Thr	Ala	Gln	Glu	Arg	Leu	Asp	Gln	Gly	Gly	Gly	Ser	Leu	Gly	Pro
				80					85					90
Gly	Ala	Ile	Ala	Ala	Ile	Val	Ile	Ala	Ala	Leu	Leu	Ala	Thr	Cys
				95					100					105
Val	Val	Leu	Ala	Leu	Val	Val	Val	Ala	Leu	Arg	Lys	Phe	Ser	Ala
				110					115					120

Ser

<210> 355

<211> 2134

<212> DNA

<213> Homo sapiens

<400> 355

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 gttggccggc ggccgggccc gacgggcatg gccctgctgc tgtgcctggt 100

gtgcctgacg gcggcgctgg cccacggctg tctgcactgc cacagcaact 150
tctccaagaa gttctccttc taccgccacc atgtgaactt caagtcctgg 200
tggttgggcg acatccccgt gtcaggggcg ctgctcaccg actggagcga 250
cgacacgatg aaggagctgc acctggccat ccccgccaag atcaccggg 300
agaagctgga ccaagtggcg acagcagtgt accagatgat ggatcagctg 350
taccagggga agatgtactt ccccggtat ttcccaacg agctgcgaaa 400
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acctggcacc aggcagctgg ggaggaggcg agctctccag ggagggaccc 500
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tgctccatct cacgtgggg gtcaacctgg ggacccttc cctccgggcc 650
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tggcatcttc cagtacgaga ccctctctg caacaactgc acagactcgc 750
acgtcgctg ctttggtat aactgcgagt agggctcagg catcacacc 800
accgtgcca gggccctact gtccctgggg tcccaggctc tccttgagg 850
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tggaagtcag ctgtccaggg cctcctgaac tacataaata actggcacia 1000
gtaagtcccc tcctcaaacc aacacaggca gtgtgtgtat gtgagcacct 1050
cgtgggtgag tatgtgtgg gcacaggctg gctccctcag ctcccacgtc 1100
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 ctgcgggatg tgattaaagt ccctgatgtt tctc 2134

<210> 356

<211> 157

<212> PRT

<213> Homo sapiens

<400> 356

Met	Ala	Leu	Leu	Leu	Cys	Leu	Val	Cys	Leu	Thr	Ala	Ala	Leu	Ala
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His	Gly	Cys	Leu	His	Cys	His	Ser	Asn	Phe	Ser	Lys	Lys	Phe	Ser
				20					25					30
Phe	Tyr	Arg	His	His	Val	Asn	Phe	Lys	Ser	Trp	Trp	Val	Gly	Asp
				35					40					45
Ile	Pro	Val	Ser	Gly	Ala	Leu	Leu	Thr	Asp	Trp	Ser	Asp	Asp	Thr
				50					55					60
Met	Lys	Glu	Leu	His	Leu	Ala	Ile	Pro	Ala	Lys	Ile	Thr	Arg	Glu
				65					70					75
Lys	Leu	Asp	Gln	Val	Ala	Thr	Ala	Val	Tyr	Gln	Met	Met	Asp	Gln
				80					85					90
Leu	Tyr	Gln	Gly	Lys	Met	Tyr	Phe	Pro	Gly	Tyr	Phe	Pro	Asn	Glu
				95					100					105
Leu	Arg	Asn	Ile	Phe	Arg	Glu	Gln	Val	His	Leu	Ile	Gln	Asn	Ala
				110					115					120
Ile	Ile	Glu	Arg	His	Leu	Ala	Pro	Gly	Ser	Trp	Gly	Gly	Gly	Gln

	125		130		135
Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro					
	140		145		150
Ser Pro Arg Gly Asp Leu Pro					
	155				

<210> 357
 <211> 1536
 <212> DNA
 <213> Homo sapiens

<400> 357
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 ttgagaaatc ctcagatggc cctgggtgctg cccaggaacc cacgtggctc 150
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 ttgatgccac caaattgagc cgtttcattg agatcaacag cctccacatg 450
 gtgacagagt acaaccctgt gactgtgatt gggttattca acagcgtaat 500
 tcagattcat ctctctctga taatgaacaa ggcctcccca gagtatgaag 550
 agaacatgca cagataccag aaggcagcca agctcttcca ggggaagatt 600
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 catgtgcaaa acttttctga tggattccta agtggaagaa tgttgaaaga 800
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 aactcaaact tcagagacac taaacaacag gatcactagg cctgccaaac 950
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cttcttatcg tgcattcata ctctgtaagc ccattctgtaa cacacctaga 1150
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 cacatgactt acacacaaca tagttcctgc tcttttaagg ttacctaagg 1300
 gttgaaactc taccttcttt cataagcaca tgtccgtctc tgactcagga 1350
 tcaaaaacca aaggatgggt ttaaaccact ttgtgaaatt gtctttttgc 1400
 cagaagttaa aggctgtctc caagtcctg aactcagcag aaatagacca 1450
 tgtgaaaact ccattgcttg ttagcatctc caactcccta tgtaaataca 1500
 caacctgcat aataaataaa aggcaatcat gttata 1536

<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

Met	Glu	Ala	Ala	Pro	Ser	Arg	Phe	Met	Phe	Leu	Leu	Phe	Leu	Leu	1	5	10	15
Thr	Cys	Glu	Leu	Ala	Ala	Glu	Val	Ala	Ala	Glu	Val	Glu	Lys	Ser	20	25	30	
Ser	Asp	Gly	Pro	Gly	Ala	Ala	Gln	Glu	Pro	Thr	Trp	Leu	Thr	Asp	35	40	45	
Val	Pro	Ala	Ala	Met	Glu	Phe	Ile	Ala	Ala	Thr	Glu	Val	Ala	Val	50	55	60	
Ile	Gly	Phe	Phe	Gln	Asp	Leu	Glu	Ile	Pro	Ala	Val	Pro	Ile	Leu	65	70	75	
His	Ser	Met	Val	Gln	Lys	Phe	Pro	Gly	Val	Ser	Phe	Gly	Ile	Ser	80	85	90	
Thr	Asp	Ser	Glu	Val	Leu	Thr	His	Tyr	Asn	Ile	Thr	Gly	Asn	Thr	95	100	105	
Ile	Cys	Leu	Phe	Arg	Leu	Val	Asp	Asn	Glu	Gln	Leu	Asn	Leu	Glu	110	115	120	
Asp	Glu	Asp	Ile	Glu	Ser	Ile	Asp	Ala	Thr	Lys	Leu	Ser	Arg	Phe	125	130	135	
Ile	Glu	Ile	Asn	Ser	Leu	His	Met	Val	Thr	Glu	Tyr	Asn	Pro	Val	140	145	150	
Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val	Ile	Gln	Ile	His	Leu	Leu	155	160	165	

Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	His	
				170					175					180	
Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly	Lys	Ile	Leu	Phe	
				185					190					195	
Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser	
				200					205					210	
Phe	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala	Ile	Tyr	
				215					220					225	
Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val	
				230					235					240	
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly	
				245					250					255	
Lys	Leu	Leu	Lys	Glu	Asn	Arg	Glu	Ser	Glu	Gly	Lys	Thr	Pro	Lys	
				260					265					270	

Val Glu Leu

<210> 359
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 359
 ccagcagtgc ccatactcca tagc 24

<210> 360
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 360
 tgacgagtgg gatacactgc 20

<210> 361
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 361
 gctctacgga aacttctgct gtgg 24

<210> 362
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 362
attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363
<211> 1777
<212> DNA
<213> Homo sapiens

<400> 363
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cctcagcggg gacccgggct cagggacgcg gcggcggcgg cggcgactgc 150
agtggctgga cgatggcagc gtccgccgga gccggggcgg tgattgcagc 200
cccagacagc cggcgctggc tgtggtcggg gctggcggcg gcgcttgggc 250
tcttgacagc tggagtatca gccttggaag tatatacgcc aaaagaaatc 300
ttcgtggcaa atggtacaca agggaagctg acctgcaagt tcaagtctac 350
tagtacgact ggccgggtga cctcagcttc ctggagcttc cagccagagg 400
gggccgacac tactgtgtcg tttttccact actccaagg gcaagtgtac 450
cttggggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500
tgacaagaaa gatgcatcaa tcaacataga aaatatgcag ttatatacaca 550
atggcaccta tatctgtgat gtcaaaaacc ctctgacat cgttgtccag 600
cctggacaca ttaggctcta tgtcgtagaa aaagagaatt tgctgtgtgt 650
tccagtttgg gtägtggtgg gcatagttac tgctgtggtc ctaggtctca 700
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gcaggctcct cggaagtccc cctccgacac tgagggtcct gttaaagagtc 850
tgccttctgg atctcaccag ggcccagtca tatatgcaca gttagaccac 900
tccggcggac atcacagtga caagattaac aagtcagagt ctgtggtgta 950
tgcggatatc cgaaagaatt aagagaatac ctagaacata tcctcagcaa 1000

gaaacaaaac caaactggac tctcgtgcag aaaatgtagc ccattaccac 1050
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 cgtggagagt aaaaagtatc ggtttta 1777

<210> 364

<211> 269

<212> PRT

<213> Homo sapiens

<400> 364

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Ser	Arg	Arg	Trp	Leu	Trp	Ser	Val	Leu	Ala	Ala	Ala	Leu	Gly	Leu
				20					25					30
Leu	Thr	Ala	Gly	Val	Ser	Ala	Leu	Glu	Val	Tyr	Thr	Pro	Lys	Glu
				35					40					45
Ile	Phe	Val	Ala	Asn	Gly	Thr	Gln	Gly	Lys	Leu	Thr	Cys	Lys	Phe
				50					55					60
Lys	Ser	Thr	Ser	Thr	Thr	Gly	Gly	Leu	Thr	Ser	Val	Ser	Trp	Ser
				65					70					75
Phe	Gln	Pro	Glu	Gly	Ala	Asp	Thr	Thr	Val	Ser	Phe	Phe	His	Tyr
				80					85					90

Ser	Gln	Gly	Gln	Val	Tyr	Leu	Gly	Asn	Tyr	Pro	Pro	Phe	Lys	Asp	95	100	105
Arg	Ile	Ser	Trp	Ala	Gly	Asp	Leu	Asp	Lys	Lys	Asp	Ala	Ser	Ile	110	115	120
Asn	Ile	Glu	Asn	Met	Gln	Phe	Ile	His	Asn	Gly	Thr	Tyr	Ile	Cys	125	130	135
Asp	Val	Lys	Asn	Pro	Pro	Asp	Ile	Val	Val	Gln	Pro	Gly	His	Ile	140	145	150
Arg	Leu	Tyr	Val	Val	Glu	Lys	Glu	Asn	Leu	Pro	Val	Phe	Pro	Val	155	160	165
Trp	Val	Val	Val	Gly	Ile	Val	Thr	Ala	Val	Val	Leu	Gly	Leu	Thr	170	175	180
Leu	Leu	Ile	Ser	Met	Ile	Leu	Ala	Val	Leu	Tyr	Arg	Arg	Lys	Asn	185	190	195
Ser	Lys	Arg	Asp	Tyr	Thr	Gly	Cys	Ser	Thr	Ser	Glu	Ser	Leu	Ser	200	205	210
Pro	Val	Lys	Gln	Ala	Pro	Arg	Lys	Ser	Pro	Ser	Asp	Thr	Glu	Gly	215	220	225
Leu	Val	Lys	Ser	Leu	Pro	Ser	Gly	Ser	His	Gln	Gly	Pro	Val	Ile	230	235	240
Tyr	Ala	Gln	Leu	Asp	His	Ser	Gly	Gly	His	His	Ser	Asp	Lys	Ile	245	250	255
Asn	Lys	Ser	Glu	Ser	Val	Val	Tyr	Ala	Asp	Ile	Arg	Lys	Asn		260	265	

<210> 365

<211> 1321

<212> DNA

<213> Homo sapiens

<400> 365

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ccatcagegc gccgggctgc cgcctctcgg ccacggctgg gtcggggggc 150
tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200
aggggcgcgg ccccggcgca gtccccgcg gccccgacc ctgaggcgtc 250
gcctctggcc gagccgccac aggagcagtc cctcgccccg tggctctccg 300
agaccccggc gccgcctgc tccaggtgct tcgccagagc catcgagagc 350
agccgcgacc tgctgcacag gatcaaggat gaggtggggc caccgggcat 400

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agtgggttgga gtttctgtag atggaaaaga agtctggtca gaaggtttag 450
 gttatgctga tggtgagaac cgtgtaccat gtaaaccaga gacagttatg 500
 cgaattgcta gcatcagcaa aagtctcacc atggttgctc ttgccaaatt 550
 gtgggaagca gggaaactgg atcttgatat tccagtacaa cattatgttc 600
 ccgaattccc agaaaaagaa tatgaagggtg aaaagggttc tgtcacaaca 650
 agattactga tttcccatTT aagtggaatt cgtcattatg aaaaggacat 700
 aaaaaagggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750
 agaatgttgc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800
 gatTTTacta aatttaaaac agagcaggag aatgaagcca aatgccggaa 850
 ttcaaaacct ggcaagaaaa agaattgattt tgaacaaggc gaattatatt 900
 tgagagaaaa gtttgaaaat tcaattgaat ccctaagatt atttaaaaat 950
 gatcctttgt tcttcaaacc tggtagtcag tttttgtatt caacttttgg 1000
 ctatacccta ctggcagcca tagtagagag agcttcagga tgtaaattatt 1050
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 aagtcaaatt ttctttgttt ccattccaaa atcaacctgc cacattttgg 1250
 gagcttttct acatgtctgt tttctcatct gtaaagtga ggaagtaaaa 1300
 catgtttata aagtaaaaaa a 1321

<210> 366

<211> 373

<212> PRT

<213> Homo sapiens

<400> 366

Met	Tyr	Arg	Leu	Leu	Ser	Ala	Val	Thr	Ala	Arg	Ala	Ala	Ala	Pro
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Gly	Gly	Leu	Ala	Ser	Ser	Cys	Gly	Arg	Arg	Gly	Val	His	Gln	Arg
				20				25						30
Ala	Gly	Leu	Pro	Pro	Leu	Gly	His	Gly	Trp	Val	Gly	Gly	Leu	Gly
				35				40						45
Leu	Gly	Leu	Gly	Leu	Ala	Leu	Gly	Val	Lys	Leu	Ala	Gly	Gly	Leu
				50				55						60

Arg Gly Ala Ala	Pro Ala Gln Ser Pro	Ala Ala Pro Asp Pro	Glu
	65	70	75
Ala Ser Pro Leu	Ala Glu Pro Pro Gln	Glu Gln Ser Leu Ala	Pro
	80	85	90
Trp Ser Pro Gln	Thr Pro Ala Pro Pro	Cys Ser Arg Cys Phe	Ala
	95	100	105
Arg Ala Ile Glu	Ser Ser Arg Asp Leu	Leu His Arg Ile Lys	Asp
	110	115	120
Glu Val Gly Ala	Pro Gly Ile Val Val	Gly Val Ser Val Asp	Gly
	125	130	135
Lys Glu Val Trp	Ser Glu Gly Leu Gly	Tyr Ala Asp Val Glu	Asn
	140	145	150
Arg Val Pro Cys	Lys Pro Glu Thr Val	Met Arg Ile Ala Ser	Ile
	155	160	165
Ser Lys Ser Leu	Thr Met Val Ala Leu	Ala Lys Leu Trp Glu	Ala
	170	175	180
Gly Lys Leu Asp	Leu Asp Ile Pro Val	Gln His Tyr Val Pro	Glu
	185	190	195
Phe Pro Glu Lys	Glu Tyr Glu Gly Glu	Lys Val Ser Val Thr	Thr
	200	205	210
Arg Leu Leu Ile	Ser His Leu Ser Gly	Ile Arg His Tyr Glu	Lys
	215	220	225
Asp Ile Lys Lys	Val Lys Glu Glu Lys	Ala Tyr Lys Ala Leu	Lys
	230	235	240
Met Met Lys Glu	Asn Val Ala Phe Glu	Gln Glu Lys Glu Gly	Lys
	245	250	255
Ser Asn Glu Lys	Asn Asp Phe Thr Lys	Phe Lys Thr Glu Gln	Glu
	260	265	270
Asn Glu Ala Lys	Cys Arg Asn Ser Lys	Pro Gly Lys Lys Lys	Asn
	275	280	285
Asp Phe Glu Gln	Gly Glu Leu Tyr Leu	Arg Glu Lys Phe Glu	Asn
	290	295	300
Ser Ile Glu Ser	Leu Arg Leu Phe Lys	Asn Asp Pro Leu Phe	Phe
	305	310	315
Lys Pro Gly Ser	Gln Phe Leu Tyr Ser	Thr Phe Gly Tyr Thr	Leu
	320	325	330
Leu Ala Ala Ile	Val Glu Arg Ala Ser	Gly Cys Lys Tyr Leu	Asp
	335	340	345

Tyr Met Gln Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val
350 355 360

Gln Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg
365 370

<210> 367

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 367

tggaagaa gtctggcag aaggttagg 30

<210> 368

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 368

catttgctt cattctctg ctctg 25

<210> 369

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 369

aaaacctcag aacaactcat ttgacacc 28

<210> 370

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 370

gtctcaccat gggtgctctt gccaaattgt gggaagcagg g 41

<210> 371

<211> 1150

<212> DNA

<213> Homo sapiens

<400> 371

gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

gaattcggct cgaggctggt gggaagaagc cgagatggcg gcagccagcg 100
 ctggggcaac ccggctgctc ctgctcttgc tgatggcggt agcagcgccc 150
 agtcgagccc ggggcagcgg ctgccgggcc gggactgggtg cgcgaggggc 200
 tggggcgga ggtcgagagg gcgaggcctg tggcacgggtg gggctgctgc 250
 tggagcactc atttgagatc gatgacagtg ccaacttccg gaagcggggc 300
 tcactgctct ggaaccagca ggatggtacc ttgtccctgt cacagcgga 350
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 gaagctgggtg gctatgtctc ctcctttgtc cctgcgtgct ccctggtgga 500
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 ttgtgtggca gtttattaaa ctgtcccca gatcgacacg caaaaaaaaa 1150

<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

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Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys
				20					25					30

Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu	35	40	45
Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe	50	55	60
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu	65	70	75
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu	80	85	90
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn	95	100	105
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp	110	115	120
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys	125	130	135
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val	140	145	150
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro	155	160	165
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu	170	175	180
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly	185	190	195
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala	200	205	210
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys	215	220	225
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser	230	235	240
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly	245	250	255
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu		260	265	

<210> 373

<211> 1706

<212> DNA

<213> Homo sapiens

<400> 373

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tgtaggcctc ctggcctcct gcctggggct ggaactgtca agatgccggg 200
ctaaaccccc tggaagggcc tgcagcaatc cctccttcct tcggtttcaa 250
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 gactgacttt gtgactgtcc tgtggtttct cctgccattg ctttgtgttt 1600
 gggaggacat gatgggggtg atggactgga aagaagggtgc caaaagttcc 1650
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 aaaaaa 1706

<210> 374

<211> 450

<212> PRT

<213> Homo sapiens

<400> 374

Met	Leu	Val	Thr	Ala	Tyr	Leu	Ala	Phe	Val	Gly	Leu	Leu	Ala	Ser	1	5	10	15
Cys	Leu	Gly	Leu	Glu	Leu	Ser	Arg	Cys	Arg	Ala	Lys	Pro	Pro	Gly	20	25	30	
Arg	Ala	Cys	Ser	Asn	Pro	Ser	Phe	Leu	Arg	Phe	Gln	Leu	Asp	Phe	35	40	45	
Tyr	Gln	Val	Tyr	Phe	Leu	Ala	Leu	Ala	Ala	Asp	Trp	Leu	Gln	Ala	50	55	60	
Pro	Tyr	Leu	Tyr	Lys	Leu	Tyr	Gln	His	Tyr	Tyr	Phe	Leu	Glu	Gly	65	70	75	
Gln	Ile	Ala	Ile	Leu	Tyr	Val	Cys	Gly	Leu	Ala	Ser	Thr	Val	Leu	80	85	90	
Phe	Gly	Leu	Val	Ala	Ser	Ser	Leu	Val	Asp	Trp	Leu	Gly	Arg	Lys	95	100	105	
Asn	Ser	Cys	Val	Leu	Phe	Ser	Leu	Thr	Tyr	Ser	Leu	Cys	Cys	Leu	110	115	120	
Thr	Lys	Leu	Ser	Gln	Asp	Tyr	Phe	Val	Leu	Leu	Val	Gly	Arg	Ala	125	130	135	
Leu	Gly	Gly	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Ser	Ala	Phe	Glu	Ala	140	145	150	
Trp	Tyr	Ile	His	Glu	His	Val	Glu	Arg	His	Asp	Phe	Pro	Ala	Glu	155	160	165	
Trp	Ile	Pro	Ala	Thr	Phe	Ala	Arg	Ala	Ala	Phe	Trp	Asn	His	Val	170	175	180	
Leu	Ala	Val	Val	Ala	Gly	Val	Ala	Ala	Glu	Ala	Val	Ala	Ser	Trp	185	190	195	
Ile	Gly	Leu	Gly	Pro	Val	Ala	Pro	Phe	Val	Ala	Ala	Ile	Pro	Leu	200	205	210	

Leu	Ala	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Arg	Asn	Trp	Gly	Glu	Asn	
				215					220					225	
Tyr	Asp	Arg	Gln	Arg	Ala	Phe	Ser	Arg	Thr	Cys	Ala	Gly	Gly	Leu	
				230					235					240	
Arg	Cys	Leu	Leu	Ser	Asp	Arg	Arg	Val	Leu	Leu	Leu	Gly	Thr	Ile	
				245					250					255	
Gln	Ala	Leu	Phe	Glu	Ser	Val	Ile	Phe	Ile	Phe	Val	Phe	Leu	Trp	
				260					265					270	
Thr	Pro	Val	Leu	Asp	Pro	His	Gly	Ala	Pro	Leu	Gly	Ile	Ile	Phe	
				275					280					285	
Ser	Ser	Phe	Met	Ala	Ala	Ser	Leu	Leu	Gly	Ser	Ser	Leu	Tyr	Arg	
				290					295					300	
Ile	Ala	Thr	Ser	Lys	Arg	Tyr	His	Leu	Gln	Pro	Met	His	Leu	Leu	
				305					310					315	
Ser	Leu	Ala	Val	Leu	Ile	Val	Val	Phe	Ser	Leu	Phe	Met	Leu	Thr	
				320					325					330	
Phe	Ser	Thr	Ser	Pro	Gly	Gln	Glu	Ser	Pro	Val	Glu	Ser	Phe	Ile	
				335					340					345	
Ala	Phe	Leu	Leu	Ile	Glu	Leu	Ala	Cys	Gly	Leu	Tyr	Phe	Pro	Ser	
				350					355					360	
Met	Ser	Phe	Leu	Arg	Arg	Lys	Val	Ile	Pro	Glu	Thr	Glu	Gln	Ala	
				365					370					375	
Gly	Val	Leu	Asn	Trp	Phe	Arg	Val	Pro	Leu	His	Ser	Leu	Ala	Cys	
				380					385					390	
Leu	Gly	Leu	Leu	Val	Leu	His	Asp	Ser	Asp	Arg	Lys	Thr	Gly	Thr	
				395					400					405	
Arg	Asn	Met	Phe	Ser	Ile	Cys	Ser	Ala	Val	Met	Val	Met	Ala	Leu	
				410					415					420	
Leu	Ala	Val	Val	Gly	Leu	Phe	Thr	Val	Val	Arg	His	Asp	Ala	Glu	
				425					430					435	
Leu	Arg	Val	Pro	Ser	Pro	Thr	Glu	Glu	Pro	Tyr	Ala	Pro	Glu	Leu	
				440					445					450	

<210> 375

<211> 1098

<212> DNA

<213> Homo sapiens

<400> 375

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 gctccccgcg tgcgtcgcgg ccacaggctt ccgtatccat gattatttgt 150
 actttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200
 cctgccaaag actttggtgg tatctttcac acaaggatat agcagattca 250
 ccttgctccc gctgaacctc cagaggcctg cggggaactc agcaacggtt 300
 tcttcatcca ggaccagatt gctctggtgg agaggggggg ctgctccttc 350
 ctctccaaga ctcggtggt ccaggagcac ggcgggcggg cggatgatcat 400
 ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450
 acagtaccca gcgcacagct gacatccccg cctcttctct gctcggccga 500
 gacggctaca tgatccgccg ctctctggaa cagcatgggc tgccatgggc 550
 catcatttcc atcccagtca atgtcaccag catccccacc tttgagctgc 600
 tgcaaccgcc ctggaccttc tggtagaaga gtttgtccca cattccagcc 650
 ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700
 aatttgagga tagcatctgg ggacaagtgg agccaggtag aggaaaaggg 750
 tttgggcggt gctaggctga aagggagacc acaccactgg ccttcccttc 800
 cccagggccc ccaagggtgt ctcatgctac aagaagaggc aagagacagg 850
 cccagggct tctggctaga acccgaaaca aaaggagctg aaggcaggtg 900
 gcctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950
 taccaggggt ctctgcacag tgaccttcac agcagttggt ggagtgggtt 1000
 aaagagctgg tgtttgggga ctcaataaac cctcactgac tttttagcaa 1050
 taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1098

<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

Met	Val	Pro	Gly	Ala	Ala	Gly	Trp	Cys	Cys	Leu	Val	Leu	Trp	Leu
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Pro	Ala	Cys	Val	Ala	Ala	His	Gly	Phe	Arg	Ile	His	Asp	Tyr	Leu
				20				25					30	
Tyr	Phe	Gln	Val	Leu	Ser	Pro	Gly	Asp	Ile	Arg	Tyr	Ile	Phe	Thr
				35				40					45	

Ala	Thr	Pro	Ala	Lys	Asp	Phe	Gly	Gly	Ile	Phe	His	Thr	Arg	Tyr	
				50					55					60	
Glu	Gln	Ile	His	Leu	Val	Pro	Ala	Glu	Pro	Pro	Glu	Ala	Cys	Gly	
				65					70					75	
Glu	Leu	Ser	Asn	Gly	Phe	Phe	Ile	Gln	Asp	Gln	Ile	Ala	Leu	Val	
				80					85					90	
Glu	Arg	Gly	Gly	Cys	Ser	Phe	Leu	Ser	Lys	Thr	Arg	Val	Val	Gln	
				95					100					105	
Glu	His	Gly	Gly	Arg	Ala	Val	Ile	Ile	Ser	Asp	Asn	Ala	Val	Asp	
				110					115					120	
Asn	Asp	Ser	Phe	Tyr	Val	Glu	Met	Ile	Gln	Asp	Ser	Thr	Gln	Arg	
				125					130					135	
Thr	Ala	Asp	Ile	Pro	Ala	Leu	Phe	Leu	Leu	Gly	Arg	Asp	Gly	Tyr	
				140					145					150	
Met	Ile	Arg	Arg	Ser	Leu	Glu	Gln	His	Gly	Leu	Pro	Trp	Ala	Ile	
				155					160					165	
Ile	Ser	Ile	Pro	Val	Asn	Val	Thr	Ser	Ile	Pro	Thr	Phe	Glu	Leu	
				170					175					180	
Leu	Gln	Pro	Pro	Trp	Thr	Phe	Trp								
				185											

<210> 377

<211> 496

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 396

<223> unknown base

<400> 377

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ctgaacaaga tggtaagca agtgactggg aaaatgccca tcctctccta 150
ctggccctac ggctgtcact gcggactagg tggcagaggc caacccaaag 200
atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg 250
aagacccagg ggtgcggcat ctacaaggac aacaacaaaa gcagcataca 300
ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350
tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400

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aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 496

<210> 378

<211> 116

<212> PRT

<213> Homo sapiens

<400> 378

Met	Glu	Leu	Ala	Leu	Leu	Cys	Gly	Leu	Val	Val	Met	Ala	Gly	Val
1				5				10					15	

Ile	Pro	Ile	Gln	Gly	Gly	Ile	Leu	Asn	Leu	Asn	Lys	Met	Val	Lys
			20					25					30	

Gln	Val	Thr	Gly	Lys	Met	Pro	Ile	Leu	Ser	Tyr	Trp	Pro	Tyr	Gly
			35					40					45	

Cys	His	Cys	Gly	Leu	Gly	Gly	Arg	Gly	Gln	Pro	Lys	Asp	Ala	Thr
			50					55					60	

Asp	Trp	Cys	Cys	Gln	Thr	His	Asp	Cys	Cys	Tyr	Asp	His	Leu	Lys
			65					70					75	

Thr	Gln	Gly	Cys	Gly	Ile	Tyr	Lys	Asp	Asn	Asn	Lys	Ser	Ser	Ile
			80					85					90	

His	Cys	Met	Asp	Leu	Ser	Gln	Arg	Tyr	Cys	Leu	Met	Ala	Val	Phe
			95					100					105	

Asn	Val	Ile	Tyr	Leu	Glu	Asn	Glu	Asp	Ser	Glu
			110					115		

<210> 379

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 379

ctgcctccac tgctctgtgc tggg 24

<210> 380

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 380

cagagcagtg gatgttcccc tggg 24

<210> 381

<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 381
ctgaacaaga tgggtcaagca agtgactggg aaaatgccca tcctc 45

<210> 382
<211> 764
<212> DNA
<213> Homo sapiens

<400> 382
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ggcgatgtgg aggggtgccg gcacaaccag acgcccagtc acaggcgaga 100
gccctgggat gcaccggcca gaggccatgc tgctgctgct cacgcttgcc 150
ctcctggggg gcccacctg ggcaggggaag atgtatggcc ctggaggagg 200
caagtatttc agcaccactg aagactacga ccatgaaatc acaggggctgc 250
gggtgtctgt aggtcttctc ctgggtgaaaa gtgtccaggt gaaacttgga 300
gactcctggg acgtgaaact gggagcctta ggtgggaata cccaggaagt 350
caccctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400
ctttcctccg gggatatggc atgtacacca gcaaggaccg ctatttctat 450
tttggaagc ttgatggcca gatctcctct gcctaccca gccaaagagg 500
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ccagttaatc tcacatactc agcaaactca cccgtgggtc gctaggggtg 650
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actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750
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<210> 383
<211> 178
<212> PRT
<213> Homo sapiens

<400> 383
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1 5 10 15

Leu	Gly	Gly	Pro	Thr	Trp	Ala	Gly	Lys	Met	Tyr	Gly	Pro	Gly	Gly	
				20					25					30	
Gly	Lys	Tyr	Phe	Ser	Thr	Thr	Glu	Asp	Tyr	Asp	His	Glu	Ile	Thr	
				35					40					45	
Gly	Leu	Arg	Val	Ser	Val	Gly	Leu	Leu	Leu	Val	Lys	Ser	Val	Gln	
				50					55					60	
Val	Lys	Leu	Gly	Asp	Ser	Trp	Asp	Val	Lys	Leu	Gly	Ala	Leu	Gly	
				65					70					75	
Gly	Asn	Thr	Gln	Glu	Val	Thr	Leu	Gln	Pro	Gly	Glu	Tyr	Ile	Thr	
				80					85					90	
Lys	Val	Phe	Val	Ala	Phe	Gln	Ala	Phe	Leu	Arg	Gly	Met	Val	Met	
				95					100					105	
Tyr	Thr	Ser	Lys	Asp	Arg	Tyr	Phe	Tyr	Phe	Gly	Lys	Leu	Asp	Gly	
				110					115					120	
Gln	Ile	Ser	Ser	Ala	Tyr	Pro	Ser	Gln	Glu	Gly	Gln	Val	Leu	Val	
				125					130					135	
Gly	Ile	Tyr	Gly	Gln	Tyr	Gln	Leu	Leu	Gly	Ile	Lys	Ser	Ile	Gly	
				140					145					150	
Phe	Glu	Trp	Asn	Tyr	Pro	Leu	Glu	Glu	Pro	Thr	Thr	Glu	Pro	Pro	
				155					160					165	
Val	Asn	Leu	Thr	Tyr	Ser	Ala	Asn	Ser	Pro	Val	Gly	Arg			
				170					175						

<210> 384

<211> 2379

<212> DNA

<213> Homo sapiens

<400> 384

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atacagatgt ggcagctcag gtagccccaa attgcctgga agaatacatc 150
atgtttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc 200
cccctcccca cccccaaaa aaactgtaaa gatgcaaaaa cgtaatatcc 250
atgaagatcc tattacctag gaagattttg atgttttgct gcgaatgcgg 300
tgttgggatt tatttgttct tggagtgttc tgcgtggctg gcaaagaata 350
atgttccaaa atcgggtccat ctccaagggt gtccaatttt tcttcctggg 400
tgtcagcgag cctgactca ctacagtga gctgacaggg gctgtcatgc 450

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aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat 500
acaaaggatg ggtttcaatg taattaggct actgagcgga tcagctgtag 550
cactggttat agccccact gtcttactga caatgctttc ttctgccgaa 600
cgaggatgcc ctaagggctg taggtgtgaa ggcaaaatgg tatattgtga 650
atctcagaaa ttacaggaga taccctcaag tataatctgct ggttgcttag 700
gtttgtccct tcgctataac agccttcaaa aacttaagta taatcaattt 750
aaagggctca accagctcac ctggctatac cttgaccata accatatcag 800
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 aaataccaca atcaatgtga agcttgaact ccggtttaat ataataccta 2300
 ttgtataaga ccctttactg attccattaa tgtcgcattt gttttaagat 2350
 aaaacttctt tcataggtaa aaaaaaaaa 2379

<210> 385
 <211> 513
 <212> PRT
 <213> Homo sapiens

<400> 385
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 20 25 30
 Glu Arg Gly Cys Pro Lys Gly Cys Arg Cys Glu Gly Lys Met Val
 35 40 45
 Tyr Cys Glu Ser Gln Lys Leu Gln Glu Ile Pro Ser Ser Ile Ser
 50 55 60
 Ala Gly Cys Leu Gly Leu Ser Leu Arg Tyr Asn Ser Leu Gln Lys
 65 70 75
 Leu Lys Tyr Asn Gln Phe Lys Gly Leu Asn Gln Leu Thr Trp Leu
 80 85 90
 Tyr Leu Asp His Asn His Ile Ser Asn Ile Asp Glu Asn Ala Phe
 95 100 105
 Asn Gly Ile Arg Arg Leu Lys Glu Leu Ile Leu Ser Ser Asn Arg
 110 115 120
 Ile Ser Tyr Phe Leu Asn Asn Thr Phe Arg Pro Val Thr Asn Leu
 125 130 135
 Arg Asn Leu Asp Leu Ser Tyr Asn Gln Leu His Ser Leu Gly Ser
 140 145 150

Glu Gln Phe Arg	Gly Leu Arg Lys Leu	Leu Ser Leu His Leu Arg
	155	160 165
Ser Asn Ser Leu Arg	Thr Ile Pro Val	Arg Ile Phe Gln Asp Cys
	170	175 180
Arg Asn Leu Glu	Leu Leu Asp Leu Gly	Tyr Asn Arg Ile Arg Ser
	185	190 195
Leu Ala Arg Asn	Val Phe Ala Gly Met	Ile Arg Leu Lys Glu Leu
	200	205 210
His Leu Glu His	Asn Gln Phe Ser Lys	Leu Asn Leu Ala Leu Phe
	215	220 225
Pro Arg Leu Val	Ser Leu Gln Asn Leu	Tyr Leu Gln Trp Asn Lys
	230	235 240
Ile Ser Val Ile	Gly Gln Thr Met Ser	Trp Thr Trp Ser Ser Leu
	245	250 255
Gln Arg Leu Asp	Leu Ser Gly Asn Glu	Ile Glu Ala Phe Ser Gly
	260	265 270
Pro Ser Val Phe	Gln Cys Val Pro Asn	Leu Gln Arg Leu Asn Leu
	275	280 285
Asp Ser Asn Lys	Leu Thr Phe Ile Gly	Gln Glu Ile Leu Asp Ser
	290	295 300
Trp Ile Ser Leu	Asn Asp Ile Ser Leu	Ala Gly Asn Ile Trp Glu
	305	310 315
Cys Ser Arg Asn	Ile Cys Ser Leu Val	Asn Trp Leu Lys Ser Phe
	320	325 330
Lys Gly Leu Arg	Glu Asn Thr Ile Ile	Cys Ala Ser Pro Lys Glu
	335	340 345
Leu Gln Gly Val	Asn Val Ile Asp Ala	Val Lys Asn Tyr Ser Ile
	350	355 360
Cys Gly Lys Ser	Thr Thr Glu Arg Phe	Asp Leu Ala Arg Ala Leu
	365	370 375
Pro Lys Pro Thr	Phe Lys Pro Lys Leu	Pro Arg Pro Lys His Glu
	380	385 390
Ser Lys Pro Pro	Leu Pro Pro Thr Val	Gly Ala Thr Glu Pro Gly
	395	400 405
Pro Glu Thr Asp	Ala Asp Ala Glu His	Ile Ser Phe His Lys Ile
	410	415 420
Ile Ala Gly Ser	Val Ala Leu Phe Leu	Ser Val Leu Val Ile Leu
	425	430 435

Leu Val Ile Tyr Val Ser Trp Lys Arg Tyr Pro Ala Ser Met Lys
440 445 450

Gln Leu Gln Gln Arg Ser Leu Met Arg Arg His Arg Lys Lys Lys
455 460 465

Arg Gln Ser Leu Lys Gln Met Thr Pro Ser Thr Gln Glu Phe Tyr
470 475 480

Val Asp Tyr Lys Pro Thr Asn Thr Glu Thr Ser Glu Met Leu Leu
485 490 495

Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu
500 505 510

Cys Glu Val

<210> 386

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 386

ctgggatctg aacagtttcg gggc 24

<210> 387

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 387

ggtccccagg acatggtctg tccc 24

<210> 388

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 388

gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389

<211> 1449

<212> DNA

<213> Homo sapiens

<400> 389

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ctcggacctc ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200
aacaccctaa tggctggtat atctggatcc tcctgctgct ggttttgggtg 250
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caacctgatt ttaggtgtgg attatcaatt taaagtatta acgacatctg 550
taattccaaa acatcaaatt taggaatagt tatttcagtt gttggaaatg 600
tccagagatc tattcatata gtctgaggaa ggacaattcg acaaaagaat 650
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aggcttttga tgtgtcactg ctgtatcata cttttatgct acacaaccaa 750
attaatgctt ctccactagt atccaaacag gcaacaatta ggtgctggaa 800
gtagtttcca tcacatttag gactccactg cagtatacag cacaccattt 850
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taacaatagc ccaagccgag aatccaacat gtccagaacc agaaccagaa 950
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tggagttgaa gggtaaagga taaatgaaga ggaaaaggaa aagattacaa 1050
gtctcagcaa aaacaagagg ttttatgcc caacctgaag aggaagaaat 1100
tgtagataga aggtgaagga gattgctgaa gatatagagc acatataatg 1150
ccaacacggg gagaaaagaa aatttcccct ttacagtaa tgaatgtggc 1200
ctccatagtc catagtgttt ctctggagcc tcagggcttg gcatttattg 1250
cagcatcatg ctaagaacct tcggcatagg tatctgttcc catgaggact 1300
gcagaagtag caatgagaca tcttcaagtg gcattttggc agtggccatc 1350
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<210> 390
<211> 146
<212> PRT
<213> Homo sapiens

<400> 390
Met Ser Arg Ser Arg Leu Phe Ser Val Thr Ser Ala Ile Ser Thr
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Ile Gly Ile Leu Cys Leu Pro Leu Phe Gln Leu Val Leu Ser Asp
20 25 30
Leu Pro Cys Glu Glu Asp Glu Met Cys Val Asn Tyr Asn Asp Gln
35 40 45
His Pro Asn Gly Trp Tyr Ile Trp Ile Leu Leu Leu Leu Val Leu
50 55 60
Val Ala Ala Leu Leu Cys Gly Ala Val Val Leu Cys Leu Gln Cys
65 70 75
Trp Leu Arg Arg Pro Arg Ile Asp Ser His Arg Arg Thr Met Ala
80 85 90
Val Phe Ala Val Gly Asp Leu Asp Ser Ile Tyr Gly Thr Glu Ala
95 100 105
Ala Val Ser Pro Thr Val Gly Ile His Leu Gln Thr Gln Thr Pro
110 115 120
Asp Leu Tyr Pro Val Pro Ala Pro Cys Phe Gly Pro Leu Gly Ser
125 130 135
Pro Pro Pro Tyr Glu Glu Ile Val Lys Thr Thr
140 145

<210> 391
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 391
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<210> 392
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 392

ccaaaacatg gagcaggaac agg 23

<210> 393

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

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<210> 394

<211> 2340

<212> DNA

<213> Homo sapiens

<400> 394

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gacgcagctg acgcccgtt attagctctc gctgcgtcgc cccggctcag 150
aagctccgtg gcggcggcga ccgtgacgag aagcccacgg ccagctcagt 200
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ttttcaagtc ttgatttgtg gcttacctca agttaccatt tttcagtcaa 400
gtctgtttgt ttgcttcttc agaaatgttt tttacaatct caagaaaaaa 450
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<211> 140
 <212> PRT
 <213> Homo sapiens

<400> 395

Met	Phe	Phe	Thr	Ile	Ser	Arg	Lys	Asn	Met	Ser	Gln	Lys	Leu	Ser	1	5	10	15
Leu	Leu	Leu	Leu	Val	Phe	Gly	Leu	Ile	Trp	Gly	Leu	Met	Leu	Leu	20	25	30	
His	Tyr	Thr	Phe	Gln	Gln	Pro	Arg	His	Gln	Ser	Ser	Val	Lys	Leu	35	40	45	
Arg	Glu	Gln	Ile	Leu	Asp	Leu	Ser	Lys	Arg	Tyr	Val	Lys	Ala	Leu	50	55	60	
Ala	Glu	Glu	Asn	Lys	Asn	Thr	Val	Asp	Val	Glu	Asn	Gly	Ala	Ser	65	70	75	
Met	Ala	Gly	Tyr	Ala	Asp	Leu	Lys	Arg	Thr	Ile	Ala	Val	Leu	Leu	80	85	90	
Asp	Asp	Ile	Leu	Gln	Arg	Leu	Val	Lys	Leu	Glu	Asn	Lys	Val	Asp	95	100	105	
Tyr	Ile	Val	Val	Asn	Gly	Ser	Ala	Ala	Asn	Thr	Thr	Asn	Gly	Thr	110	115	120	
Ser	Gly	Asn	Leu	Val	Pro	Val	Thr	Thr	Asn	Lys	Arg	Thr	Asn	Val	125	130	135	
Ser	Gly	Ser	Ile	Arg	140													

<210> 396
 <211> 2639
 <212> DNA
 <213> Homo sapiens

<400> 396

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 accttcggcc ttttcgacag cttcagcctg actcgggtgg attgtagcgg 200
 cctgggcccc cacatcatgc cggtgcccat ccctctggac acagcccact 250
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 gggccggggt acacgacgtt ggctggcctg gatctcagcc acaacctgct 350
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<210> 397

<211> 353

<212> PRT

<213> Homo sapiens

<400> 397

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Thr	Thr	Arg	Pro	Cys	Phe	Pro	Gly	Cys	Gln	Cys	Glu	Val	Glu	Thr
				20					25					30
Phe	Gly	Leu	Phe	Asp	Ser	Phe	Ser	Leu	Thr	Arg	Val	Asp	Cys	Ser
				35					40					45
Gly	Leu	Gly	Pro	His	Ile	Met	Pro	Val	Pro	Ile	Pro	Leu	Asp	Thr
				50					55					60
Ala	His	Leu	Asp	Leu	Ser	Ser	Asn	Arg	Leu	Glu	Met	Val	Asn	Glu
				65					70					75
Ser	Val	Leu	Ala	Gly	Pro	Gly	Tyr	Thr	Thr	Leu	Ala	Gly	Leu	Asp
				80					85					90

Leu Ser His Asn	Leu Leu Thr Ser Ile	Ser Pro Thr Ala Phe Ser
95	100	105
Arg Leu Arg Tyr	Leu Glu Ser Leu Asp	Leu Ser His Asn Gly Leu
110	115	120
Thr Ala Leu Pro	Ala Glu Ser Phe Thr	Ser Ser Pro Leu Ser Asp
125	130	135
Val Asn Leu Ser	His Asn Gln Leu Arg	Glu Val Ser Val Ser Ala
140	145	150
Phe Thr Thr His	Ser Gln Gly Arg Ala	Leu His Val Asp Leu Ser
155	160	165
His Asn Leu Ile	His Arg Leu Val Pro	His Pro Thr Arg Ala Gly
170	175	180
Leu Pro Ala Pro	Thr Ile Gln Ser Leu	Asn Leu Ala Trp Asn Arg
185	190	195
Leu His Ala Val	Pro Asn Leu Arg Asp	Leu Pro Leu Arg Tyr Leu
200	205	210
Ser Leu Asp Gly	Asn Pro Leu Ala Val	Ile Gly Pro Gly Ala Phe
215	220	225
Ala Gly Leu Gly	Gly Leu Thr His Leu	Ser Leu Ala Ser Leu Gln
230	235	240
Arg Leu Pro Glu	Leu Ala Pro Ser Gly	Phe Arg Glu Leu Pro Gly
245	250	255
Leu Gln Val Leu	Asp Leu Ser Gly Asn	Pro Lys Leu Asn Trp Ala
260	265	270
Gly Ala Glu Val	Phe Ser Gly Leu Ser	Ser Leu Gln Glu Leu Asp
275	280	285
Leu Ser Gly Thr	Asn Leu Val Pro Leu	Pro Glu Ala Leu Leu Leu
290	295	300
His Leu Pro Ala	Leu Gln Ser Val Ser	Val Gly Gln Asp Val Arg
305	310	315
Cys Arg Arg Leu	Val Arg Glu Gly Thr	Tyr Pro Arg Arg Pro Gly
320	325	330
Ser Ser Pro Lys	Val Pro Leu His Cys	Val Asp Thr Arg Glu Ser
335	340	345
Ala Ala Arg Gly	Pro Thr Ile Leu	
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<210> 398

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

ccctgccagc cgagagcttc acc 23

<210> 399

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 399

ggttggtgcc cgaaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 400

caaccccaag cttaactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

gatggcgag ccacagcttc tgtgagattc gatttctccc cagttcccct 50

gtgggtctga ggggaccaga agggtagact acgttggtt tctggaaggg 100

gaggctatat ggcgtcaattc cccaaaacaa gttttgacat ttcccctgaa 150

atgtcattct ctatctattc actgcaagtg cctgctgttc caggccttac 200

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cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300

ttctcttcac gggaggcttg gcagtttttc ttactcctgt ggtctccaga 350

tttcaggcct aagatgaaag cctctagtct tgccttcagc cttctctctg 400

ctgcgtttta tctcctatgg actccttcca ctggactgaa gacactcaat 450

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 ccaaaaaaaaa aaaaaaaaaa a 1571

<210> 402

<211> 261

<212> PRT

<213> Homo sapiens

<400> 402

Met	Arg	Gln	Phe	Pro	Lys	Thr	Ser	Phe	Asp	Ile	Ser	Pro	Glu	Met
1				5					10				15	

Ser	Phe	Ser	Ile	Tyr	Ser	Leu	Gln	Val	Pro	Ala	Val	Pro	Gly	Leu
				20				25					30	

Thr	Cys	Trp	Ala	Leu	Thr	Ala	Glu	Pro	Gly	Trp	Gly	Gln	Asn	Lys
				35				40					45	

Gly	Ala	Thr	Thr	Cys	Ala	Thr	Asn	Ser	His	Ser	Asp	Ser	Glu	Leu	50	55	60
Arg	Pro	Glu	Ile	Phe	Ser	Ser	Arg	Glu	Ala	Trp	Gln	Phe	Phe	Leu	65	70	75
Leu	Leu	Trp	Ser	Pro	Asp	Phe	Arg	Pro	Lys	Met	Lys	Ala	Ser	Ser	80	85	90
Leu	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr	95	100	105
Pro	Ser	Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile	110	115	120
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg	125	130	135
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu	140	145	150
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys	155	160	165
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe	170	175	180
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser	185	190	195
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu	200	205	210
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys	215	220	225
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln	230	235	240
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln	245	250	255
Trp	Met	Glu	Glu	Thr	Glu										260		

<210> 403

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

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<210> 404
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 404
agtcctcctt aagattctga tgtcaa 26

<210> 405
<211> 998
<212> DNA
<213> Homo sapiens

<400> 405
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aggcttttgc cgctgaccca gagatggccc cgagcgagca aattcctact 100
gtccggctgc gcggtaccg tggccgagct agcaaccttt cccctggatc 150
tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200
ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250
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cacccgccat ttacagacac gtagtgtatt ctggaggctg aatggtcaca 350
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caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850
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<210> 406
<211> 323
<212> PRT
<213> Homo sapiens

<400> 406

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Arg	Trp	Pro	Arg	Ala	Ser	Lys	Phe	Leu	Leu	Ser	Gly	Cys	Ala	Ala
				20					25					30
Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr
				35					40					45
Arg	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp
				50					55					60
Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala
				65					70					75
Leu	Gly	Ile	Ile	Glu	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly
				80					85					90
Val	Thr	Pro	Ala	Ile	Tyr	Arg	His	Val	Val	Tyr	Ser	Gly	Gly	Arg
				95					100					105
Met	Val	Thr	Tyr	Glu	His	Leu	Arg	Glu	Val	Val	Phe	Gly	Lys	Ser
				110					115					120
Glu	Asp	Glu	His	Tyr	Pro	Leu	Trp	Lys	Ser	Val	Ile	Gly	Gly	Met
				125					130					135
Met	Ala	Gly	Val	Ile	Gly	Gln	Phe	Leu	Ala	Asn	Pro	Thr	Asp	Leu
				140					145					150
Val	Lys	Val	Gln	Met	Gln	Met	Glu	Gly	Lys	Arg	Lys	Leu	Glu	Gly
				155					160					165
Lys	Pro	Leu	Arg	Phe	Arg	Gly	Val	His	His	Ala	Phe	Ala	Lys	Ile
				170					175					180
Leu	Ala	Glu	Gly	Gly	Ile	Arg	Gly	Leu	Trp	Ala	Gly	Trp	Val	Pro
				185					190					195
Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr
				200					205					210
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu
				215					220					225
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu
				230					235					240
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg
				245					250					255

Ile Met Asn Gln Pro Arg Asp Lys Gln Gly Arg Gly Leu Leu Tyr		
	260	265 270
Lys Ser Ser Thr Asp Cys Leu Ile Gln Ala Val Gln Gly Glu Gly		
	275	280 285
Phe Met Ser Leu Tyr Lys Gly Phe Leu Pro Ser Trp Leu Arg Met		
	290	295 300
Thr Pro Trp Ser Met Val Phe Trp Leu Thr Tyr Glu Lys Ile Arg		
	305	310 315
Glu Met Ser Gly Val Ser Pro Phe		
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<210> 407

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 407

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<210> 408

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 408

gcggaattct taaaatggac tgactccact catc 34

<210> 409

<211> 1487

<212> DNA

<213> Homo sapiens

<400> 409

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tcctgcgcgc gcgcctgaag tcggcgtggg cgtttgagga agctgggata 100

cagcatttaa tgaaaaattt atgcttaaga agtaaaaatg gcaggcttcc 150

tagataattt tcgttgcca gaatgtgaat gtattgactg gaggtagaga 200

agaaatgctg tggcatctgt tgtcgcaggt atattgtttt ttacaggctg 250

gtggataatg attgatgcag ctgtggtgta tcctaagcca gaacagttga 300

accatgcctt tcacacatgt ggtgtatttt ccacattggc tttcttcatg 350

ataaatgctg tatccaatgc tcaggtgaga ggtgatagct atgaaagcgg 400
 ctgttttagga agaacagggtg ctcgagtttg gcttttcatt ggtttcatgt 450
 tgatgttttg gtcacttatt gcttccatgt ggattctttt tgggtgcatat 500
 gttacccaaa atactgatgt ttatccggga ctagctgtgt tttttcaaaa 550
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 gctcatgcct gtaatcccag cactttggga ggccgaggcg ggccgattgc 1000
 ttgaggtcaa gtgtttgaga ccagcctggc caacatggcg aaaccccatc 1050
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 cagctacctg ggaggctgag gcaggagaat cgcttgaacc cggggggcag 1150
 aggttgcagt gagctgagtt tgcgccactg cactctagcc tgggggagaa 1200
 agtgaaactc cctctcaaaa aaaagaccac tctcagtatc tctgatttct 1250
 gaagatgtac aaaaaaatat agcttcatat atctggaatg agcactgagc 1300
 cataaaagggt tttcagcaag ttgtaactta ttttggccta aaaatgaggt 1350
 ttttttggtg aagaaaaaat atttgttctt atgtattgaa gaagtgtact 1400
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<210> 410
 <211> 158
 <212> PRT
 <213> Homo sapiens

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 Ile Asp Trp Ser Glu Arg Arg Asn Ala Val Ala Ser Val Val Ala
 20 25 30

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				35					40					45	
Val	Val	Tyr	Pro	Lys	Pro	Glu	Gln	Leu	Asn	His	Ala	Phe	His	Thr	
				50					55					60	
Cys	Gly	Val	Phe	Ser	Thr	Leu	Ala	Phe	Phe	Met	Ile	Asn	Ala	Val	
				65					70					75	
Ser	Asn	Ala	Gln	Val	Arg	Gly	Asp	Ser	Tyr	Glu	Ser	Gly	Cys	Leu	
				80					85					90	
Gly	Arg	Thr	Gly	Ala	Arg	Val	Trp	Leu	Phe	Ile	Gly	Phe	Met	Leu	
				95					100					105	
Met	Phe	Gly	Ser	Leu	Ile	Ala	Ser	Met	Trp	Ile	Leu	Phe	Gly	Ala	
				110					115					120	
Tyr	Val	Thr	Gln	Asn	Thr	Asp	Val	Tyr	Pro	Gly	Leu	Ala	Val	Phe	
				125					130					135	
Phe	Gln	Asn	Ala	Leu	Ile	Phe	Phe	Ser	Thr	Leu	Ile	Tyr	Lys	Phe	
				140					145					150	
Gly	Arg	Thr	Glu	Glu	Leu	Trp	Thr								
				155											

<210> 411
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 411
 gtttgaggaa gctgggatac 20

<210> 412
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 412
 ccaaactcga gcacctgttc 20

<210> 413
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 413
atggcaggct tcctagataa ttttcgttgg ccagaatgtg 40

<210> 414
<211> 1337
<212> DNA
<213> Homo sapiens

<400> 414
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actgcatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150
gggaggtggg actgtcagaa gctggcccag ggtggtggtc agctgggtca 200
gggacctacg gcacctgctg gaccacctcg ccttctccat cgaagcaggg 250
aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccacccttc 300
acctggacag gatgagagtg tcaggtgtgc ttgcctcctt ggccctcatc 350
tttgccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400
catgaaaacc atccgtctgc cacgctggct ggagcctcg cccaccaagg 450
agatccaggt taaaaagtac aagtgtggcc tcatcaagcc ctgcccagcc 500
aactactttg cgtttaaaat ctgcagtggg gccgccaacg tcgtgggccc 550
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tgggcagagg cctaaacatc gccctggtga atggaaccac gggagctgtg 650
ctgggacaga aggcatttga catgtactct ggagatgtta tgcacctagt 700
gaaattcctt aaagaaattc cggggggtgc actggtgctg gtggcctcct 750
acgacgatcc agggaccaa atgaacgatg aaagcaggaa actcttctct 800
gacttgggga gttcctacgc aaaacaactg ggcttccggg acagctgggt 850
cttcatagga gccaaagacc tcaggggtaa aagcccttt gagcagttct 900
taaagaacag ccagacaca aacaaatagc agggatggcc agagctgctg 950
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 tatttttgct ggttttgaaa aaaaaaaaaa aaaaaaaa 1337

<210> 415
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 415

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Ile	Val	Thr	Thr	Trp	Met	Phe	Ile	Arg	Ser	Tyr	Met	Ser	Phe	Ser	20	25	30	
Met	Lys	Thr	Ile	Arg	Leu	Pro	Arg	Trp	Leu	Ala	Ala	Ser	Pro	Thr	35	40	45	
Lys	Glu	Ile	Gln	Val	Lys	Lys	Tyr	Lys	Cys	Gly	Leu	Ile	Lys	Pro	50	55	60	
Cys	Pro	Ala	Asn	Tyr	Phe	Ala	Phe	Lys	Ile	Cys	Ser	Gly	Ala	Ala	65	70	75	
Asn	Val	Val	Gly	Pro	Thr	Met	Cys	Phe	Glu	Asp	Arg	Met	Ile	Met	80	85	90	
Ser	Pro	Val	Lys	Asn	Asn	Val	Gly	Arg	Gly	Leu	Asn	Ile	Ala	Leu	95	100	105	
Val	Asn	Gly	Thr	Thr	Gly	Ala	Val	Leu	Gly	Gln	Lys	Ala	Phe	Asp	110	115	120	
Met	Tyr	Ser	Gly	Asp	Val	Met	His	Leu	Val	Lys	Phe	Leu	Lys	Glu	125	130	135	
Ile	Pro	Gly	Gly	Ala	Leu	Val	Leu	Val	Ala	Ser	Tyr	Asp	Asp	Pro	140	145	150	
Gly	Thr	Lys	Met	Asn	Asp	Glu	Ser	Arg	Lys	Leu	Phe	Ser	Asp	Leu	155	160	165	
Gly	Ser	Ser	Tyr	Ala	Lys	Gln	Leu	Gly	Phe	Arg	Asp	Ser	Trp	Val	170	175	180	
Phe	Ile	Gly	Ala	Lys	Asp	Leu	Arg	Gly	Lys	Ser	Pro	Phe	Glu	Gln	185	190	195	
Phe	Leu	Lys	Asn	Ser	Pro	Asp	Thr	Asn	Lys	Tyr	Glu	Gly	Trp	Pro	200	205	210	
Glu	Leu	Leu	Glu	Met	Glu	Gly	Cys	Met	Pro	Pro	Lys	Pro	Phe	215	220			

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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 416
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<210> 417
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 417
ggatggccag agctgctg 18

<210> 418
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 418
aaagtacaag tgtggcctca tcaagc 26

<210> 419
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 419
tctgactcct aagtcaggca ggag 24

<210> 420
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 420
attctctcca cagacagctg gttc 24

<210> 421

<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 421
gtacaagtgt ggcctcatca agccctgccc agccaactac tttgcg 46

<210> 422
<211> 1701
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1528
<223> unknown base

<400> 422
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tgtcctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc 100
tggaagccca cagagacaga gacagcaaga gaagcagaga taaatacact 150
cacgccagga gctcgctcgc tctctctctc tctctctcac tcctccctcc 200
ctctctctct gcctgtccta gtccctctagt cctcaaattc ccagtcccct 250
gcaccccttc ctgggacact atgttgttct ccgccctcct gctggagggtg 300
atttggatcc tggctgcaga tgggggtcaa cactggacgt atgagggcc 350
acatggtcag gaccattggc cagcctctta ccctgagtgt ggaaacaatg 400
cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450
ttgcctgctc tgcagcccca cggatatgac cagcctggca ccgagccttt 500
ggacctgcac aacaatggcc acacagtgc actctctctg ccctctaccc 550
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 t 1701

<210> 423
 <211> 337
 <212> PRT
 <213> Homo sapiens

<400> 423
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 20 25 30
 Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln
 35 40 45
 Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp
 50 55 60
 Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu
 65 70 75
 Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu
 80 85 90

Pro Ser Thr Leu Tyr Leu Gly Gly Leu	Pro Arg Lys Tyr Val Ala
95	100 105
Ala Gln Leu His Leu His Trp Gly Gln Lys Gly Ser Pro Gly Gly	
110	115 120
Ser Glu His Gln Ile Asn Ser Glu Ala Thr Phe Ala Glu Leu His	
125	130 135
Ile Val His Tyr Asp Ser Asp Ser Tyr Asp Ser Leu Ser Glu Ala	
140	145 150
Ala Glu Arg Pro Gln Gly Leu Ala Val Leu Gly Ile Leu Ile Glu	
155	160 165
Val Gly Glu Thr Lys Asn Ile Ala Tyr Glu His Ile Leu Ser His	
170	175 180
Leu His Glu Val Arg His Lys Asp Gln Lys Thr Ser Val Pro Pro	
185	190 195
Phe Asn Leu Arg Glu Leu Leu Pro Lys Gln Leu Gly Gln Tyr Phe	
200	205 210
Arg Tyr Asn Gly Ser Leu Thr Thr Pro Pro Cys Tyr Gln Ser Val	
215	220 225
Leu Trp Thr Val Phe Tyr Arg Arg Ser Gln Ile Ser Met Glu Gln	
230	235 240
Leu Glu Lys Leu Gln Gly Thr Leu Phe Ser Thr Glu Glu Glu Pro	
245	250 255
Ser Lys Leu Leu Val Gln Asn Tyr Arg Ala Leu Gln Pro Leu Asn	
260	265 270
Gln Arg Met Val Phe Ala Ser Phe Ile Gln Ala Gly Ser Ser Tyr	
275	280 285
Thr Thr Gly Glu Met Leu Ser Leu Gly Val Gly Ile Leu Val Gly	
290	295 300
Cys Leu Cys Leu Leu Leu Ala Val Tyr Phe Ile Ala Arg Lys Ile	
305	310 315
Arg Lys Lys Arg Leu Glu Asn Arg Lys Ser Val Val Phe Thr Ser	
320	325 330
Ala Gln Ala Thr Thr Glu Ala	
335	

<210> 424

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 424
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<210> 425
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 425
cccgatctgc ctgctgta 18

<210> 426
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 426
ctgcactgta tggccattat tgtg 24

<210> 427
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 427
cagaaaccca tgatacccta ctgaacaccg aatcccctgg aagcc 45

<210> 428
<211> 1073
<212> DNA
<213> Homo sapiens

<400> 428
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aacctgcttt gggactccct cccacaaaac tggctccgga tcagggaaca 200
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<210> 429

<211> 209

<212> PRT

<213> Homo sapiens

<400> 429

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Ser	Leu	Pro	Gln	Leu	Lys	Pro	Ala	Leu	Gly	Leu	Pro	Pro	Thr	Lys
			20						25					30
Leu	Ala	Pro	Asp	Gln	Gly	Thr	Leu	Pro	Asn	Gln	Gln	Gln	Ser	Asn
			35						40					45
Gln	Val	Phe	Pro	Ser	Leu	Ser	Leu	Ile	Pro	Leu	Thr	Gln	Met	Leu
			50						55					60
Thr	Leu	Gly	Pro	Asp	Leu	His	Leu	Leu	Asn	Pro	Ala	Ala	Gly	Met
			65						70					75
Thr	Pro	Gly	Thr	Gln	Thr	His	Pro	Leu	Thr	Leu	Gly	Gly	Leu	Asn
			80						85					90
Val	Gln	Gln	Gln	Leu	His	Pro	His	Val	Leu	Pro	Ile	Phe	Val	Thr

	95	100	105
Gln Leu Gly Ala	Gln Gly Thr Ile Leu	Ser Ser Glu Glu Leu	Pro
	110	115	120
Gln Ile Phe Thr	Ser Leu Ile Ile His	Ser Leu Phe Pro Gly Gly	
	125	130	135
Ile Leu Pro Thr	Ser Gln Ala Gly Ala	Asn Pro Asp Val Gln Asp	
	140	145	150
Gly Ser Leu Pro	Ala Gly Gly Ala Gly	Val Asn Pro Ala Thr Gln	
	155	160	165
Gly Thr Pro Ala	Gly Arg Leu Pro Thr	Pro Ser Gly Thr Asp Asp	
	170	175	180
Asp Phe Ala Val	Thr Thr Pro Ala Gly	Ile Gln Arg Ser Thr His	
	185	190	195
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	200	205	

<210> 430

<211> 1257

<212> DNA

<213> Homo Sapien

<400> 430

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ccgcctccag ctccgcgtg cccggcagcc gggagccatg cgaccccagg 150
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tgaagaacta ccaaaaataaa tgctttaatt ttcatttgct acctcttttt 900
ttattatgcc ttggaatggt tcaacttaaata gacattttta ataagtttat 950
gtatacatct gaatgaaaag caaagctaaa tatgtttaca gaccaaagtg 1000
tgatttcaca ctgtttttta atctagcatt attcattttg cttcaatcaa 1050
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35 40 45
Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
50 55 60
Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
65 70 75
Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
80 85 90
Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
95 100 105
Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
110 115 120
Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
125 130 135

Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg
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Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu
				155					160					165
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln
				170					175					180
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser
				185					190					195
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp
				200					205					210
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp
				215					220					225
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